

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: June 9, 2005, 15:27:47 ; Search time 583 Seconds
(without alignments)
2275.470 Million cell updates/sec

Title: US-10-812-620-2
Perfect score: 1179
Sequence: 1 MNSTKSPASHHTGCGFKNS.....IPCFYSPWPCMEPISPLD 214

Scoring table:
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 6046767 seqs, 3099530249 residues

Total number of hits satisfying chosen parameters: 12093534

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-DB=Published Applications_NA -QFMT=fastap -SUFFIX=p2n.rnpb -MINMATCH=0.1
-LOOPCU=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blomsum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10812620 @CGN 1 1 624 @runat_07062005_124340_3366
-NCPU=6 -ICPU=3 -NO_WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:
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11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq*
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14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq*
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16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq*
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21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq*
22: /cgn2_6/ptodata/1/pubpna/US10J_PUBCOMB.seq*
23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq*
24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq*
25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq*
26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1149	97.5	2517	21	US-10-812-620-1
2	774	96.8	9	9	US-09-965-529-40
3	774	96.8	9	9	US-09-969-680A-40
4	774	96.8	9	9	US-09-909-320-376
5	774	96.8	9	9	US-09-909-088B-376
6	774	96.8	9	9	US-09-905-291A-376
7	774	96.8	9	9	US-09-902-853-376
8	774	96.8	9	9	US-09-907-824-376
9	774	96.8	9	9	US-09-907-841-376
10	774	96.8	9	10	US-09-904-011-376
11	774	96.8	9	10	US-09-903-640-376
12	774	96.8	9	10	US-09-908-093-376
13	774	96.8	9	10	US-09-906-742-376
14	774	96.8	9	10	US-09-906-838-376
15	774	96.8	9	10	US-09-907-613-376
16	774	96.8	9	10	US-09-907-942-376
17	774	96.8	9	10	US-09-904-859-376
18	774	96.8	9	10	US-09-909-204-376
19	774	96.8	9	10	US-09-904-820-376
20	774	96.8	9	10	US-09-904-786-376
21	774	96.8	9	10	US-09-906-646-376
22	774	96.8	9	10	US-09-906-700-376
23	774	96.8	9	10	US-09-903-786-376
24	774	96.8	9	10	US-09-902-903-376
25	774	96.8	9	10	US-09-903-749A-376
26	774	96.8	9	10	US-09-904-119-376
27	774	96.8	9	10	US-09-904-956-376
28	774	96.8	9	10	US-09-902-736-376
29	774	96.8	9	10	US-09-907-794-376
30	774	96.8	9	10	US-09-903-943-376
31	774	96.8	9	10	US-09-904-462-376
32	774	96.8	9	10	US-09-907-925-376
33	774	96.8	9	10	US-09-902-692-376
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36	774	96.8	9	10	US-09-909-064-376
37	774	96.8	9	10	US-09-904-553-376
38	774	96.8	9	10	US-09-905-381-376
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41	774	96.8	9	10	US-09-905-088-376
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45	774	96.8	9	10	US-09-902-634-376

ALIGNMENTS

RESULT 1
US-10-812-620-1
; Sequence 1, Application: US/10812620
; Publication No. US20050019860A1
; GENERAL INFORMATION:
; APPLICANT: Japan Science and Technology Corporation
; TITLE OF INVENTION: A novel C-type lectin and its genes
; FILE REFERENCE: J9404071
; CURRENT APPLICATION NUMBER: US/10/812,620
; CURRENT FILING DATE: 2004-03-29
; PRIOR APPLICATION NUMBER: US/10/110,945
; PRIOR FILING DATE: 2002-04-14
; PRIOR APPLICATION NUMBER: JP 11-293724
; PRIOR FILING DATE: 1999-10-15
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 1

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; LENGTH: 2517
; TYPE: DNA
; ORGANISM: Mouse
US-10-812-620-1

Alignment Scores:
Pred. No.: 1.4e-135 Length: 2517
Score: 1149.00 Matches: 209
Percent Similarity: 98.13% Conservative: 1
Best Local Similarity: 97.66% Mismatches: 4
Query Match: 97.46% Indels: 0
DB: 21 Gaps: 0

US-10-812-620-2 (1-214) x US-10-812-620-1 (1-2517)

QY 1 MetAenSerThrLysSerProAlaSerHisThrGluArgGlyCysPheLysAenSer 20
Db 124 ATGAATTCACCAAAATCGGCTGCATCCACACACAGAGAGGATGCTTCAAAAACCTCC 183
QY 21 GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle 40
Db 184 CAAGTGTCTCTCGACAGATAGCCGGGGCTCATCTCTGTTCTCAGTGGCTGTTTCATC 243
QY 41 ThrArgCysValValThrTyrArgSerSerGlnIleSerGlyGlnAsnLeuGlnProHis 60
Db 244 ACCAGATGTGTGTAACATATCGACGCTCTCAAAATTCGGGGCAGAACTTACAGCCACAT 303
QY 61 ArgAsnIleLysGluLeuSerCysTyrSerGluAlaSerGlySerValLysAenCysCys 80
Db 304 AGAAATATTAAGAGAGCTTTCCTGCTACAGTGGGATCAGGTTTCAGTCAAGAAATGCTGT 363
QY 81 ProLeuAsnTrpLysHisTyrGlnSerSerCysTyrPhePheSerThrThrThrLeuThr 100
Db 364 CCTTTGAATCGAAACATATCAATCTAGTGTGTTATTTTCTCTACGACAACTTGACC 423
QY 101 TrpSerSerSerLeuLysAenCysSerAspMetGlyAlaHisLeuValValIleAspThr 120
Db 424 TGGTCATCAAGTTTAAAGAAATGCTCAGACATGGGGGCTCACTGGTGGTTATCGACACA 483
QY 121 GlnGluGlnGlnPheLeuPheArgThrLysProLysArgLysGluPheTyrIleGly 140
Db 484 CAGGAAGAGCAGAGAAATCTCTTTTCGCACAAAAATCTAAAGAGAAAGAGTTTATATGGA 543
QY 141 LeuThrAspGlnValValGluGlyGlnTrpGlnTrpValAspAspThrProPheThrGlu 160
Db 544 CTGACACAGCAGGTGGTGGAGGTCAGTGGCAATGGAGGATGATACACTTTTCACAGAG 603
QY 161 SerLeuSerPheTrpAspAlaGlyGluProAsnAsnIleValLeuValGluAspCysAla 180
Db 604 TCCTTGACCTTCTGGGATGCTGGGAGGCCCAACATATAGTTTGGTGGAGGACTGTGCC 663
QY 181 ThrIleArgAspSerSerAenSerArgLysAenTrpAenAspIleProCysPheTyrSer 200
Db 664 ACCATAAGGAGACTCTTCAAACTCCAGGAAGAACTGGAATGATAAATCCCTGTTTCTACAGT 723
QY 201 MetProTrpIleCysGluMetProGluIleSerProLeuAsp 214
Db 724 ATGCCCTTGGATTTGTGAGATGCCAGAAATAAGTCTCTCAGGAC 765

RESULT 2
US-09-965-529-40
; Sequence 40, Application US/09965529
; Publication No. US20020182671A1
; GENERAL INFORMATION:
; APPLICANT: LAL, Preeti
; APPLICANT: YUE, Henry
; APPLICANT: TANG, Y. Tom
; APPLICANT: BANDMAN, Olga
; APPLICANT: BURFORD, Neil
; APPLICANT: AZIMZAI, Yalda
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: LU, Dying Aina M.
; APPLICANT: PATTERSON, Chandra
```

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; Sequence 40, Application US/09969680A
; Publication No. US20030124649A1
; GENERAL INFORMATION:
; APPLICANT: LAL, Preeti; YUE, Henry
; APPLICANT: TANG, Y. Tom; BANDMAN, Olga
; APPLICANT: BUEFORD, Neil; AZIMZAI, Yalda
; APPLICANT: BAUGHN, Marian R.; LU, Dying Aina M.
; APPLICANT: PATTERSON, Chandra
; TITLE OF INVENTION: MEMBRANE ASSOCIATED PROTEINS
; FILE REFERENCE: PF-0731-1 USA
; CURRENT APPLICATION NUMBER: US/09/969,680A
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US00/22315
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/149,641
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/164,203
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PERL Program
; SEQ ID NO 40
; LENGTH: 968
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030124649A1 1521513CB1
US-09-969-680A-40

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Pred. No.: 2,82e-88 Length: 968
Score: 774.00 Matches: 143
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Best Local Similarity: 66.51% Mismatches: 43
Query Match: 65.65% Indels: 2
DB: 10 Gaps: 2

US-10-812-620-2 (1-214) x US-09-969-680A-40 (1-968)

Qy 1 MetaSerThrLysSerProAlaSerHisThrGluArgGlyCysPheLysAsnSer 20
Db 162 ATGAATTCATCTAATCATCTGAACCAATGCGACAGAGAGATGCTTC---TCITCC 218

Qy 21 GlnValLeuSerThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle 40
Db 219 CAATGTTCTATGAGCTGTGCTGGATCCCATCTATTCTCAGTGCCTGTTTCATC 278

Qy 41 ThrArgCysValValThrThrArgSerSerGlnIleSerGlyGln---AsnLeuGlnPro 59
Db 279 ACCAGATGTGTGTGACATTTGCGATCTTTCAAAACCTGTGTATGAGAAAAAGTTTCAGCTA 338

Qy 60 HisArgAsnIleLysGluLeuSerCysThrSerGluAlaSerGlySerValLysAsnCys 79
Db 339 CCTGAGAAATTTCCAGAGCTCTCTCTGTACATATTTATGATCAGGTTCAATCAAGAAATGT 398

Qy 80 CysProLeuAsnThrLysHisThrGlnSerSerCysThrPhePheSerThrThrLeu 99
Db 399 TGTCATTTGACTGGGAATATTTTCATCCAGTGTCTACTCTTCTTCTACTGACACAT 458

Qy 100 ThrTrpSerSerLeuLysAsnCysSerAspMetGlyAlaHisLeuValValIleAsp 119
Db 459 TCCTGGCGGTAAAGTTTAAAGAACTGCTCAGCCATGGGGGCTACCTGGTGGTTATCAAC 518

Qy 120 ThrGlnGluGlnGlnPheLeuPheArgThrLysProLysArgLysGluPheThrIle 139
Db 519 TCACAGAGGAGCAGGAATTCCTTTCTTACAGAAACCTAAATGAGAGAGATTTTATT 578

Qy 140 GlyLeuThrAspGlnValValGluGlnTrpGlnTrpValAspAspThrProPheThr 159
Db 579 GGACTGTGAGCCAGGTTGTGAGGGTCAGTGGCAATGGGTGGACGGCACACCTTTGACA 638

Qy 160 GluSerLeuSerPheThrAspAlaGlyGluProAsnAsnIleValLeuValGluAspCys 179
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Percent Similarity: 79.07% Conservatives: 27
Best Local Similarity: 66.51% Mismatches: 43
Query Match: 65.65% Indels: 2
DB: 9 Gaps: 2

US-10-812-620-2 (1-214) x US-09-909-088B-376 (1-997)

Qy 1 MetAsnSerThrLysSerProAlaSerHisThrGluArgGlyCysPheLysAsnSer 20
Db 106 ATGAATTCATCTAATCATCTGAAACAACATGACAGAGAGAGATGCTTC---TCTTCC 162
Qy 21 GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle 40
Db 163 CAAATGTTCTTATGGACTGTGTGGGATCCCCATCTATTCTCAGTGGCTGTTTCATC 222
Qy 41 ThrArgCysValValThrTyrArgSerSerGlnIleSerGlyGln---AsnLeuGlnPro 59
Db 223 ACCAGATGTGTGACATTCGGATCTTTCAACCTGTGATGAGAAAAGTTTCAGCTA 282
Qy 60 HisArgAsnIleLysGluLeuSerCysTyrSerGluAlaSerGlySerValLysAsnCys 79
Db 283 CCGTGAATTTTCAGAGCTCTCTCTGCTACAAATATGATGATCAGGTTTCAGTCAAGATTGT 342
Qy 80 CysProLeuAsnTrpLysHisThrGlnSerSerCysTyrPhePheSerThrThrLeu 99
Db 343 TGTCCATTTGAATGGGAATATTTTCAATCCAGCTGTCTTCTTTCTACTGCACCATTT 402
Qy 100 ThrTrpSerSerLeuLysAsnCysSerAspMetGlyAlaHisLeuValIleAsp 119
Db 403 TCCGTGGCGGTTAGTTTAAAGAACTGCTCAGCCATGGGGCTCACCTGGTGGTTATCAAC 462
Qy 120 ThrGlnGluGlnGlnPheLeuPheArgThrLysProLysArgLysGluPheTyrIle 139
Db 463 TCACAGGAGGACGAGGAATTCCTTTCTCAAGAAACCTTAAATGAGAGAGATTTTATT 522
Qy 140 GlyLeuThrAspGlnValValGluGlnTrpGlnTrpValAspAspThrProPheThr 159
Db 523 GGAATGTTCAGACACAGGTTGTCAGGGTTCAGTGGCAATGGGTGGACGACACCTTTTGACA 582
Qy 160 GluSerLeuSerPheTrpAspAlaGlyProAsnAsnIleValLeuValGluAspCys 179
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Qy 180 AlaThrIleArgAspSerSerAsnSerArgLysAsnTrpAsnAspIleProCysPheTyr 199
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Qy 200 SerMetProTrpIleCysGluMetProGluIleSerProLeuAsp 214
Db 703 AATTATTTCGGATTTCTGAAATGTTAGGAATAAATCCTTTGAAC 747

RESULT 6

US-09-905-291A-376
Sequence 376, Application US/09905291A
Patent No. US20020160374A1

GENERAL INFORMATION:

APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Deenoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kijavina, Ivar J.

APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/905,291A
CURRENT FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 376
LENGTH: 997
TYPE: DNA
ORGANISM: Homo Sapien
US-09-905-291A-376
Alignment Scores:
Pred. No.: 2,95e-88 Length: 997
Score: 774.00 Matches: 143
Percent Similarity: 79.07% Conservative: 27
Best Local Similarity: 66.51% Mismatches: 43
Query Match: 65.65% Indels: 2
DB: 9 Gaps: 2

US-10-812-620-2 (1-214) x US-09-905-291A-376 (1-997)

Qy 1 MetAsnSerThrLysSerProAlaSerHisThrGluArgGlyCysPheLysAsnSer 20
Db 106 ATGAATTCATCTAATCATCTGAAACAACATGACAGAGAGAGATGCTTC---TCTTCC 162
Qy 21 GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle 40
Db 163 CAAATGTTCTTATGGACTGTGTGGGATCCCCATCTATTCTCAGTGGCTGTTTCATC 222
Qy 41 ThrArgCysValValThrTyrArgSerSerGlnIleSerGlyGln---AsnLeuGlnPro 59

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Db 223 ACCAGATGTTGTGACATTTCCGATCTTTCAAACTGATGAGAAAAAGTTTCAGCTA 282
Qy 60 HisArgAsnIleLysGluLeuSerCysTyrSerGluAlaSerGlySerValLysAsnCys 79
Db 283 CTTGAGAAATTTACAGAGCTCTCTGCTCAATATGAGTTCAGTTCAGTCAAGAAATTTG 342
Qy 80 CysProLeuAsnTrpLysHisTyrGlnSerSerCysTyrPhePheSerThrThrThrLeu 99
Db 343 TGTCAATGAACTGGGAATATTTCAATCCAGTCTACTCTTTCTACTGACCACTT 402
Qy 100 ThrTrpSerSerSerLeuLysAsnCysSerAspMetGlyAlaHisLeuValLysLeu 119
Db 403 TCTGGCGTTAAGTTTAAAGAACTGCTCAGCATGGGGGCTCAGTGTGTGTTATCAAC 462
Qy 120 ThrGlnGluGlnGluPheLeuPheArgThrLysProLysArgLysGluPheTyrIle 139
Db 463 TCACAGGAGGAGCAGAAATCTCTTCTCAAAAGAAACCTAAATGAGAGAGTTTTTATT 522
Qy 140 GlyLeuThrAspGlnValValGluGlyGlnTrpGlnTrpValAspAspThrProPheThr 159
Db 523 GACATGTCACAGCAGGTTCTCAGGGTCAGTGGCAATGGTGGACGGCACCTTTTGACA 582
Qy 160 GluSerLeuSerPheTrpAspAlaGlyGluProAsnAsnIleValLeuValGluAspCys 179
Db 583 AAGTCTCTGAGCTCTCGGATGTAGGGAGCCCAACAACATAGCTACCTGGAGGACTGT 642
Qy 180 AlaThrIleArgAspSerSerAsnSerArgLysAsnTrpAsnAspIleProCysPheTyr 199
Db 643 GCCACCATGAGAGACTCTTCAAAACCCAGGCAAAATTTGAATGATGTAACTGTTTCTC 702
Qy 200 SerMetProTrpIleCysGluMetProGluIleSerProLeuAsp 214
Db 703 AATTATTTTCGGATTTGTGAAATGTAGGAATAAATCTTTGAAC 747
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RESULT 7

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US-09-902-853-376
; Sequence 376, Application US/09902853
; Publication No. US20020192859A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/902,853
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US/09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US 60/143,048
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; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 376
; LENGTH: 997
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-902-853-376

Alignment Scores:
Pred. No.: 2,95e-88 Length: 997
Score: 774.00 Matches: 143
Percent Similarity: 79.07% Conservative: 27
Best Local Similarity: 66.51% Mismatches: 43
Query Match: 65.65% Indels: 2
Db: 9 Gaps: 2

US-10-812-620-2 (1-214) x US-09-902-853-376 (1-997)
Qy 1 MetAsnSerThrLysSerProAlaSerHisHisThrGluArgGlyCysPheLysAsnSer 20
Db 106 ATGATTCATCTTAATCATCTGAAACACAAATGCACAGAGAGAGGATGTTCTC---TCTTCC 162
Qy 21 GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle 40
Db 163 CAATGTTCTTATGGACTGTTGCTGGGATCCCATCTATTCTCAGTGCCTGTTTCATC 222
Qy 41 ThrArgCysValValThrTyrArgSerSerGlnIleSerGlyGln---AsnLeuGlnPro 59
Db 223 ACCAGATGTTGTGACATTTTCGCAATCTTTCAAACTGATGAGAAAAAGTTTCAGCTA 282
Qy 60 HisArgAsnIleLysGluLeuSerCysTyrSerGluAlaSerGlySerValLysAsnCys 79
Db 283 CTTGAGAAATTTACAGAGCTCTCTGCTCAATATGAGTTCAGTTCAGTCAAGAAATTTG 342
Qy 80 CysProLeuAsnTrpLysHisTyrGlnSerSerCysTyrPhePheSerThrThrThrLeu 99
Db 343 TGTCAATGAACTGGGAATATTTCAATCCAGTCTACTCTTTCTACTGACCACTT 402
Qy 100 ThrTrpSerSerSerLeuLysAsnCysSerAspMetGlyAlaHisLeuValLysLeu 119
Db 403 TCTGGCGTTAAGTTTAAAGAACTGCTCAGCATGGGGGCTCAGTGTGTGTTATCAAC 462
Qy 120 ThrGlnGluGlnGluPheLeuPheArgThrLysProLysArgLysGluPheTyrIle 139
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Db 463 TCACAGGAGGACAGGAATTCCTTCCTACAGAAACCTAAATGAGAGATTTTATT 522
Qy 140 GlyLeuThrAspGlnValValGluGlnTrpGlnTrpValAspAspThrProPheThr 159
Db 523 GGACTGTTCAGACCAGGTTGTCTGAGGTCAGTGGCAATGGGTGGACGGGCACACCTTTGACA 582
Qy 160 GluSerLeuSerPheTrpAspAlaGluProAsnAsnIleValLeuValGluAspCys 179
Db 583 AAGTCTCTGAGCTTCTGGGATGTAGGGAGGCCCAACACATAGCTACCTCGAGGAGCTGT 642
Qy 180 AlaThrIleArgAspSerAsnSerArgLysAsnTrpAsnAspIleProCysPheTyr 199
Db 643 GCCACATGAGAGACTCTTCAACCCAGGAGCAATGGAAATGATGATTAACCTGTTTCCTC 702
Qy 200 SerMetProTrpIleCysGluMetProGluIleSerProLeuAsp 214
Db 703 AATTATTTCGATTTGTGAATGGTAGAATAAATCCTTTTGAC 747

RESULT 8

US-09-907-824-376
; Sequence 376, Application US/09907824
; Publication No. US20020197671A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mathet, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,824
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089

; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 376
; LENGTH: 997
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-907-824-376

Alignment Scores:
Pred. No.: 2,95e-88 Length: 997
Score: 774.00 Matches: 143
Percent Similarity: 79.07% Conservative: 27
Best Local Similarity: 66.51% Mismatches: 43
Query Match: 65.65% Indels: 2
DB: 9 Gaps: 2

US-10-812-620-2 (1-214) x US-09-907-824-376 (1-997)

Qy 1 MetaAsnSerThrLysSerProAlaSerHisThrGluArgGlyCysPheLysAsnSer 20
Db 106 ATGAATTCATCTAAATCATCTGAAACACAATGACAGAGAGAGATGCTTC---TCITCC 162
Qy 21 GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle 40
Db 163 CAAATGTTCTTATGGACTGTTGCTGGGATCCCCATCTATTTCTCAGTGCCTGTTTCATC 222
Qy 41 ThrArgCysValValThrTyrArgSerSerGlnIleSerGlyGln---AsnLeuGlnPro 59
Db 223 ACCAGATGTGTGTGACATTTTCGCATCTTTCAAACCTGTGTATGAGAAAAAGTTTCAGCTA 282
Qy 60 HisArgAsnIleLysGluLeuSerCysTyrSerGluAlaSerGlySerValLysAsnCys 79
Db 283 CCTGAGAAATTTCAACAGAGCTCTCTCTGCTACAATTTATGATCAGGTTCAAGAAATGT 342
Qy 80 CysProLeuAsnTrpLysHisTyrGlnSerSerCysTyrPhePheSerThrThrLeu 99
Db 343 TGTCATTGAACCTGGGAATATTTTCATCCAGCTGCTACTCTCTTTCTACTGACACCAT 402
Qy 100 ThrTrpSerSerSerLeuLysAsnCysSerAspMetGlyAlaHisLeuValIleAsp 119
Db 403 TCCTGGGCGTTAAGTTTAAAGAACTGCTCAGCCATGGGGCTCACCTGGTGGTTATCAAC 462
Qy 120 ThrGlnGluGlnGluPheLeuPheArgThrLysProLysArgLysGluPheTyrIle 139
Db 463 TCACAGGAGGAGCAGGAATTTCTTTCTACAAGAAACCTAAATGAGAGAGATTTTTTATT 522
Qy 140 GlyLeuThrAspGlnValValGluGlnTrpGlnTrpValAspAspThrProPheThr 159
Db 523 GGACTGTACACCCAGGTTGTGAGGGTTCAGTGGCAATGGGTGGACGGCACACCTTTGACA 582
Qy 160 GluSerLeuSerPheTrpAspAlaGlyGluProAsnAsnIleValLeuValGluAspCys 179
Db 583 AAGTCTCTGAGCTTCTGGGATGTAGGGAGGCCCAACACATAGCTACCTCGAGGAGCTGT 642
Qy 180 AlaThrIleArgAspSerSerAsnSerArgLysAsnTrpAsnAspIleProCysPheTyr 199
Db 643 GCCACCATGAGAGACTCTTCAAACCCAGGCAAAATTTGGAATGATGATTAACCTGTTTCCTC 702

Qy	200	SerMetProTrpIleCysGluMetProGluIleSerProLeuAsp	214
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Db	703	AATTATTTCGGATTTGTGAAATGGTAGGAATAAATCCTTTGAAC	747

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RESULT 9
US-09-907-841-376
; Sequence 376, Application US/09907841
; Publication No. US20020198366A1
GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,841
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; REMAINING Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 376
; LENGTH: 997
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-907-841-376

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Alignment Scores:	
Pred. No.:	2,95e-88
Score:	774.00
Percent Similarity:	79.07%
Best Local Similarity:	66.51%
Length:	997
Matches:	143
Conservative:	27
Mismatches:	43

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; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904.011
; CURRENT FILING DATE: 2001-07-11
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 376
; LENGTH: 997
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-904-011-376

Alignment Scores:
Pred. No.: 2,95e-88 Length: 997
Score: 774.00 Matches: 143
Percent Similarity: 79.07% Conservatives: 27
Best Local Similarity: 66.51% Mismatches: 43
Query Match: 65.65% Indels: 2
DB: 10 Gaps: 2

US-10-812-620-2 (1-214) x US-09-904-011-376 (1-997)

Qy 1 MethAsnSerThrLysSerProAlaSerHisThrGluArgGlyCysPheLysAsnSer 20
Db 106 ATGAATTCATCTAATCATCTGTAACACAAATGCACAGAGAGGATGCTTC---TCTTCC 162
Qy 21 GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle 40
Db 163 CAAATGTTCTATGAGACTCTGTTGGGATCCCAATCTATCTTCAGTGGCTGTTTCATC 222
Qy 41 ThrArgCysValValThrTyrArgSerSerGlnIleSerGlyGln---AsnLeuGlnPro 59

; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/904.011
; CURRENT FILING DATE: 2001-07-11
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
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; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 376
; LENGTH: 997
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-904-011-376

Alignment Scores:
Pred. No.: 2,95e-88 Length: 997
Score: 774.00 Matches: 143
Percent Similarity: 79.07% Conservatives: 27
Best Local Similarity: 66.51% Mismatches: 43
Query Match: 65.65% Indels: 2
DB: 10 Gaps: 2

US-10-812-620-2 (1-214) x US-09-904-011-376 (1-997)

Qy 1 MethAsnSerThrLysSerProAlaSerHisThrGluArgGlyCysPheLysAsnSer 20
Db 106 ATGAATTCATCTAATCATCTGTAACACAAATGCACAGAGAGGATGCTTC---TCTTCC 162
Qy 21 GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle 40
Db 163 CAAATGTTCTATGAGACTCTGTTGGGATCCCAATCTATCTTCAGTGGCTGTTTCATC 222
Qy 41 ThrArgCysValValThrTyrArgSerSerGlnIleSerGlyGln---AsnLeuGlnPro 59

; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: KJjavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/903,640
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 423
```

; SEQ ID NO 376
; LENGTH: 997
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-903-640-376

Alignment Scores:
Pred. No.: 2,95e-88 Length: 997
Score: 774.00 Matches: 143
Percent Similarity: 79.07% Conservatives: 27
Best Local Similarity: 66.51% Mismatches: 43
Query Match: 65.65% Indels: 2
DB: 10 Gaps: 2

US-10-812-620-2 (1-214) x US-09-903-640-376 (1-997)

Qy 1 MetAsnSerThrLysSerProAlaSerHisHisThrGluArgGlyCysPheLysHenSer 20
Db 106 ATGAATTTCATCTAAATCATCTCGAAACACAATGCACAGAGAGGATGCTTC---TCTTCC 162
Qy 21 GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPhe 40
Db 163 CAAATGTTCTTATGAGCTCTCTGGATGCCATCTTATCTCAGTCCTGTTTCATC 222
Qy 41 ThrArgCysValValThrTyrArgSerSerGlnIleSerGlyGln---AsnLeuGlnPro 59
Db 223 ACCAGATGTTGTGACATTCGCATCTTCAAACCTGTGATGAGAAAAAGTTTCAGCTA 282
Qy 60 HisArgAsnIleLysGluLeuSerCysTyrSerGluAlaSerGlySerValLysHenCys 79
Db 283 CCTGAGAATTTCCACAGAGCTCTCTGCTACAAATATGATGATCAGGTTTCAGTCAAGAATTGT 342
Qy 80 CysProLeuAsnTrpLysHisTyrGlnSerSerCysTyrPhePheSerThrThrThrLeu 99
Db 343 TGTCCATTGAATCGGAATATTTTCAATCCAGCTGCTACTCTTTTCTACTGACACCAT 402
Qy 100 ThrTrpSerSerSerLeuLysAsnCysSerAspMetGlyAlaHisLeuValLleAsp 119
Db 403 TCCTGGCGGTTAAAGTTTAAAGAACTGCTCAGCCATGGGGGCTCACCTGGTGTATCAAC 462
Qy 120 ThrGlnGluGlnGlnGluPheLeuPheArgThrLysProLysArgGlyGluPheTyrIle 139
Db 463 TCACAGGAGGACGAGAAATTCCTTCTTCAAGAAACCTTAAATGAGAGAGTGTATTTTAT 522
Qy 140 GlyLeuThrAspGlnValValGluGlnThrGlnTrpValAspThrProPheThr 159
Db 523 GGAGTGTTCAGACAGAGTTGTTCAGGGTTCAGTCCAAATGGTGGACGACACCTTTTGACA 582
Qy 160 GluSerLeuSerPheTrpAspAlaGlyGluProAsnAsnIleValLeuValGluAspCys 179
Db 583 AAGTCTCTGAGCTTCTGGATGTAGGGAGCCCAACATAGCTTACCTGGAGGACTGT 642
Qy 180 AlaThrIleArgAspSerSerAsnSerArgLysAsnTrpAsnAspIleProCysPheTyr 199
Db 643 GCCACCATGAGAGACTCTTCAAAACCAAGGCAAAATTTGAATGATGTAACCTGTTTCTC 702
Qy 200 SerMetProTrpIleCysGluMetProGluIleSerProLeuAsp 214
Db 703 AATTATTTTTCGATTTGTGAAATGTTAGGAATAAATCTCTTTGAAC 747

RESULT 12

US-09-908-093-376
; Sequence 376, Application US/09908093
; Publication NO. US20030017498A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kijavir, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/908,093
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 376
; LENGTH: 997
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-908-093-376

Alignment Scores:

Pred. No.: 2,95e-88 Length: 997
Score: 774.00 Matches: 143
Percent Similarity: 79.07% Conservatives: 27
Best Local Similarity: 66.51% Mismatches: 43
Query Match: 65.65% Indels: 2
DB: 10 Gaps: 2

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Qy 1 MetAenSerThrLysSerProAlaSerHisThrGluArgGlyCysPheLysAenSer 20
Db 106 ATGAATTCATCTAAATCATCTGAAACACAATGCACAGAGAGGATGCTTC--TCTTCC 162
Qy 21 GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle 40
Db 163 CAAATGTTCTTATGGACTGTTGCTGGGATCCCATCTCTATTCTCAGTGCCTGTTTCATC 222
Qy 41 ThrArgCysValValThrTyrArgSerSerGlnIleSerGlyGln---AsnLeuGlnPro 59
Db 223 ACCAGATGTGTGTGACATTTCCGATCTTCAACCTGTGTATGAGAAAAGTTTCAGCTA 282
Qy 60 HisArgAenIleLysGluLeuSerCysTyrSerGluAlaSerGlySerValLysAenCys 79
Db 283 CCTGAGAATTTCCACAGAGCTCTCTGCTACATATTATGGATCAGGTTTCAGTCAAGAAATGT 342
Qy 80 CysProLeuAenTrpLysHisTyrGlnSerSerCysTyrPhePheSerThrThrLeu 99
Db 343 TGTCCATTGAACTGGGAATATTTTCAATCCAGCTGCTACTTCTTTCTACTGCACCACT 402
Qy 100 ThrTrpSerSerLeuLysAenCysSerAspMetGlyAlaHisLeuValValIleAsp 119
Db 403 TCCCTGGGGTTAAGTTTAAAGACTGCTCACCCATGGGGGCTCACCTGGTGGTTATCAAC 462
Qy 120 ThrGlnGluGlnGluPheLeuPheArgThrLysProLysArgLysGluPheTyrIle 139
Db 463 TCACAGGAGGAGCAGGAATCTCTTCTCAAGAAACCTAAATCAGAGAGTTTTTATT 522
Qy 140 GlyLeuThrAspGlnValValGluGlyGlnTrpGlnTrpValAspAspThrProPheThr 159
Db 523 GGACTGTGCAGACCAAGTTGTCAGGGTCAGTGGCAATGGGTGGACGGCACACCTTTGACA 582
Qy 160 GluSerLeuSerPheTrpAspAlaGlyCysProAenIleValLeuValGluAspCys 179
Db 583 AAGTCTCTGAGCTTCTGGGATGTAGGGAGGCCCAACACATAGCTACCTGGAGGACTGT 642
Qy 180 AlaThrIleArgAspSerSerAsnSerArgLysAenTrpAsnAspIleProCysPheTyr 199
Db 643 GCCACCATGAGAGACTCTTCAAAACCAAGGCAAAATGGAAATGATGATTAACCTGTTTCTC 702
Qy 200 SerMetProTrpIleCysGluMetProGluIleSerProLeuAsp 214
Db 703 AATTATTTCGATTTGTGAATGGTAGGAATAAATCCTTTGAAC 747

RESULT 13
US-09-906-742-376
; Sequence 376, Application US/09906742
; Publication No. US20030023054A1
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
```

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; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/906,742
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/665,350
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
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; PRIOR FILING DATE: 1999-09-15
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; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
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; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 376
; LENGTH: 997
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-906-742-376

Alignment Scores:
Pred. No.: 2,95e-88 Length: 997
Score: 774.00 Matches: 143
Percent Similarity: 79.07% Conservative: 27
Best Local Similarity: 66.51% Mismatches: 43
Query Match: 65.65% Indels: 2
DB: 10 Gaps: 2

US-10-812-620-2 (1-214) x US-09-906-742-376 (1-997)
Qy 1 MetAenSerThrLysSerProAlaSerHisThrGluArgGlyCysPheLysAenSer 20
Db 106 ATGAATTCATCTAAATCATCTGAAACACAATGCACAGAGAGGATGCTTC--TCTTCC 162
Qy 21 GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle 40
Db 163 CAAATGTTCTTATGGACTGTTGCTGGGATCCCATCTCTATTCTCAGTGCCTGTTTCATC 222
Qy 41 ThrArgCysValValThrTyrArgSerSerGlnIleSerGlyGln---AsnLeuGlnPro 59
Db 223 ACCAGATGTGTGTGACATTTCCGATCTTCAACCTGTGTATGAGAAAAGTTTCAGCTA 282
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QY 60 HisArgAsnIleLysGluLeuSerCysTyrSerGluAlaSerGlySerValIysAsnCys 79
Db 283 CTGAGATTTTCACAGAGCTCTCTGCTACAAATATGGATCAGGTTCAAGATGTT 342
QY 80 CysProLeuAsnTrpLysHisTyrGlnSerSerCysTyrPhePheSerThrThrLeu 99
Db 343 TGTCCATTGAATCGGGAATATTTCAATCCAGCTGCTACTTCTTTCTACTGACACCAT 402
QY 100 ThrTrpSerSerSerLeuIysAsnCysSerAspMetGlyAlaHisLeuValIleAsp 119
Db 403 TCTCTGGCGTTAAGTTTAAAGAACTGCTCAGCCATGGGGGCTCACCTGGTGTATCAAC 462
QY 120 ThrGlnGluGlnGlnPheLeuPheArgThrLysProLysArgLysGluPheTyrIle 139
Db 463 TCACAGGAGGACAGGAATCTCTTCTACAGAAACCTAAATGAGAGGTTTTTATT 522
QY 140 GlyLeuThrAspGlnValValGluGlnTrpGlnTrpValAspAspThrProPheThr 159
Db 523 CGACTGTACAGACAGGTTCTGAGGGTCAGTGGCAATGGTGGACGGCACACCTTTGACA 582
QY 160 GluSerLeuSerPheTrpAspAlaGlyGluProAsnAsnIleValLeuValGluAspCys 179
Db 583 AAGTCTCTGAGCTTCGGGATGTAGGGGAGCCCAACATAGCTACCTGGAGGACTGT 642
QY 180 AlaThrIleArgAspSerSerAsnSerArgLysAsnTrpAsnAspIleProCysPheTyr 199
Db 643 GCACACATGAGAGACTCTTCAACCCAGGCCAAATTTGAATGATGTAACTGTTTCCTC 702
QY 200 SerMetProTrpIleCysGluMetProGluIleSerProLeuAsp 214
Db 703 AATTATTTCGGATTTGTGAATGGTAGGAATAAATCTCTTGAAC 747

RESULT 14

US-09-906-838-376
Sequence 376, Application US/09906838
Publication No. US20030027143A1
GENERAL INFORMATION:

APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/906,838
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07

APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/906,838
CURRENT FILING DATE: 2001-07-16
PRIOR APPLICATION NUMBER: 09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07

US-10-812-620-2 (1-214) x US-09-906-838-376 (1-997)

QY 1 MetAsnSerThrLysSerProAlaSerHisHisThrGluArgGlyCysPheLysAsnSer 20
Db 106 ATGATTCATCTAATCATCTGAAACACAATGCACAGAGAGGATGTTCC---TCTTCC 162
QY 21 GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle 40
Db 163 CAAATGTTCTTATGGACTGTTGCTGGGATCCCATCTTATTTCTCAGTGCCTGTTTCATC 222
QY 41 ThrArgCysValValThrTyrArgSerSerGlnIleSerGlyGln---AsnLeuGlnPro 59
Db 223 ACCAGATGTGTGTGACATTTCCGATCTCTTCAAACTGTGTGATGAGAAAAAGTTTCAGCTA 282
QY 60 HisArgAsnIleLysGluLeuSerCysTyrSerGluAlaSerGlySerValIysAsnCys 79
Db 283 CTGAGATTTTCACAGAGCTCTCTGCTACAAATATGGATCAGGTTCAAGATGTTGT 342
QY 80 CysProLeuAsnTrpLysHisTyrGlnSerSerCysTyrPhePheSerThrThrLeu 99
Db 343 TGTCCATTGAATCGGGAATATTTCAATCCAGCTGCTACTTCTTTCTACTGACACCAT 402
QY 100 ThrTrpSerSerSerLeuIysAsnCysSerAspMetGlyAlaHisLeuValIleAsp 119
Db 403 TCTCTGGCGTTAAGTTTAAAGAACTGCTCAGCCATGGGGGCTCACCTGGTGTATCAAC 462
QY 120 ThrGlnGluGlnGlnPheLeuPheArgThrLysProLysArgLysGluPheTyrIle 139
Db 703 AATTATTTCGGATTTGTGAATGGTAGGAATAAATCTCTTGAAC 747

Db 703 AATTATTTTCGGATTGTGAAATGGTAGGAATAAATCCTTTGAAC 747

Search completed: June 9, 2005, 17:44:27
Job time : 594 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 9, 2005, 03:50:51 ; Search time 420 Seconds
(without alignments)
9805.973 Million cell updates/sec

Title: US-10-812-620-1
Perfect score: 2517
Sequence: 1 cggctgttactcttgact.....aaataagtaataaactatt 2517

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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6: /cgn2_6/ptodata/1/ina/backfiles.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	439.4	17.5	997	4	US-09-902-775A-376
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5	439.4	17.5	997	4	US-09-903-603A-376
6	439.4	17.5	997	4	US-09-904-920A-376
7	439.4	17.5	997	4	US-09-909-064-376
8	439.4	17.5	997	4	US-09-905-361A-376
9	439.4	17.5	997	4	US-09-906-618-376
10	157.8	6.3	301	3	US-09-222-575-29
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13	157.8	6.3	301	4	US-09-339-338-29
14	157.8	6.3	301	4	US-09-433-826B-29
15	157.8	6.3	301	4	US-09-604-287A-29
16	157.8	6.3	301	4	US-09-285-480-29
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21	94.8	3.8	1104	3	US-09-111-470-1
22	94.8	3.8	1104	4	US-09-862-802A-1
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24	83.6	3.3	169334	4	US-09-949-016-15999
25	82	3.3	99370	4	US-09-949-016-12816
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27	82	3.3	144158	4	US-09-949-016-11755

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Sequence 14724, A
Sequence 14577, A
Sequence 14578, A
Sequence 41762, A
Sequence 41761, A
Sequence 15691, A
Sequence 15450, A
Sequence 12008, A
Sequence 17056, A
Sequence 15968, A
Sequence 8, Appl
Sequence 51, Appl
Sequence 16415, A
Sequence 17504, A
Sequence 14353, A
Sequence 17590, A
Sequence 14095, A

ALIGNMENTS

RESULT 1

US-09-907-794A-376

; Sequence 376, Application US/09907794A

; Patent No. 6635468

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Botstein, David

; APPLICANT: Desnovers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, A.

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth, J.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Mather, Jennie P.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William, I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: 10466-14

; CURRENT APPLICATION NUMBER: US/09/907,794A

; PRIOR FILING DATE: 2001-07-17

; PRIOR APPLICATION NUMBER: PCT/US00/04414

; PRIOR FILING DATE: 2000-02-22

; PRIOR APPLICATION NUMBER: US 60/143,048

; PRIOR FILING DATE: 1999-07-07

; PRIOR APPLICATION NUMBER: US 60/145,698

; PRIOR FILING DATE: 1999-07-26

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; PRIOR FILING DATE: 1999-09-08

; PRIOR APPLICATION NUMBER: PCT/US99/20944

; PRIOR FILING DATE: 1999-09-13

; PRIOR APPLICATION NUMBER: PCT/US99/21090

; PRIOR FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: PCT/US99/21547

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, PRIOR APPLICATION NUMBER: PCT/US99/28565
, PRIOR FILING DATE: 1999-12-02
, PRIOR APPLICATION NUMBER: PCT/US99/30095
, PRIOR FILING DATE: 1999-12-16
, PRIOR APPLICATION NUMBER: PCT/US99/30911
, PRIOR FILING DATE: 1999-12-20
, PRIOR APPLICATION NUMBER: PCT/US99/30999
, PRIOR FILING DATE: 1999-12-20
, PRIOR APPLICATION NUMBER: PCT/US00/00219
, PRIOR FILING DATE: 2000-01-05
, NUMBER OF SEQ ID NOS: 423
, SEQ ID NO 376
, LENGTH: 997
, TYPE: DNA
, ORGANISM: Homo Sapien
US-09-905-125A-376

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Query Match 17.5%; Score 439.4; DB 4; Length 997;

Best Local Similarity 72.5%; Fred. NO. 6.9E-105;
Matches 610; Conservative 0; Mismatches 216; Indels 11; Gaps 3;

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Qy	147	ATCCACCCACACAGAGAGAGGATGCTTCAAAAACTCCCAAGTGTCTCTCTCGAGCGATAGC	206
Db	129	AACACAATGCACAGAGAGAGATGCTTC---TCCTTCCCAATGTTCTTATGGAGCTGTTCG	185
Qy	207	CGGGCCCTCCATCTCTGTTTCTCAGTGGCTGTTTTCATCACAGATGTGTGTAACATATCG	266
Db	186	TGGGATCCCCATCTATTTCTCAGTGCTGTTTCATCACAGATGTGTGTGTGACATTTTCG	245
Qy	267	CAGCTCTCAAA---TTTCCGGGCGAGAACTTACAGCCACATAGAAATATTAAGGAGCTTTC	323
Db	246	CATCTTTCAAACTGTGATGAGAAAAAGTTTCAGCTACCTCAGAAATTTTCACAGAGCTCTC	305
Qy	324	CTGCTACAGTCAGGCATCAGGTCAGTCACAAGAAATGTGTCTTGTGACCTTTGTGACTCGGAACATTA	383
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Qy	384	TCAACTAGTTGTTATTTTTTCTCTACGACAACTTCGACCTGGTGCATCAAGCTTTTAAAGAA	443
Db	366	TCAACTCAGCTGCTACTTCTTTCTACTGACACCATTTCTCGGGCGTTTAAGTTTAAAGAA	425
Qy	444	TTGCTCAGACATGCGGGGCTCACCTGGTGGTTATCGACACACAGGAAGACAGGAATTCCT	503
Db	426	CTGCTCAGCCATGCGGGGCTCACCTGGTGGTTATCAACTTCACAGGAGGACAGGAATTCCT	485
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Db	486	TTCTCTACAAGAAACCTAAATGAGAGAGTTTTTTATTGGACTGTGCAGACAGGTGTGCGA	545
Qy	564	GGGTCACTGGCAATGGGAGGATGATACACCTTTACAGAGTCCCTGACCTTCTGGGATGC	623
Db	546	GGGTCACTGGCAATGGGTGGACGCGACACCTTTGACAAAGTCTCTGAGCTTCTGGGATGT	605
Qy	624	TGGGGAGCCCAACAATATAGTTTTGGTGGAGGACTGTGCGCAACCAATAGGGACTCTTCAAA	683
Db	606	AGGGGAGCCCAACAACATAGCTACCTCGGAGGACTGTGCGCAACCATGAGAGACTCTTCAAA	665
Qy	684	CTCCAGAGAGAACTGGGAATGATAATCCTGTCTTCTACAGTATGCTTTGGATTTCTGAGAT	743
Db	666	CCCAAGGCAAAATTGGGAATGATGAACCTGTCTTCTCAATTTATTTTTCGGAATTTGTGAAT	725
Qy	744	GCCAGAAATTAAGTCTCTCAGGACTAAGTGCAA-----GGAAATACAAGGGAATGGCTTAC	798
Db	726	GGTAGGAATAATCTTTTGAACAAAGGAANAATCTCTTTAAGAACAGAGGCAACATCAA	785
Qy	799	ATGCATGAAGAGAACAGAGTGAATGTATTAACAAACCAAAATCCAACTAAGAAAAATAT	858
Db	786	ATGTGTAAAGAAAGGAGCAAGAACATGGCCACACCCACCGCCCCCAACGAGAAATTTG	845

	915
Qy	859 CTATCAGGCATCAGAAGCACTGCGACATGTATGTTACTTGGGACATTAAGTAAAAAAGA
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; Sequence 376, Application US/09902775A	
; Patent No. 6686451	
902	

RESULT 3

US-09-902-775A-376
 ? Sequence 376, Application US/09902775A
 ? Patent No. 6686451
 ? GENERAL INFORMATION:
 ? APPLICANT: Genentech, Inc.
 ? APPLICANT: Ashkenazi, Avi
 ? APPLICANT: Botstein, David
 ? APPLICANT: Desnoyers, Luc
 ? APPLICANT: Eaton, Dan L.
 ? APPLICANT: Ferrara, Napoleone
 ? APPLICANT: Filvaroff, Ellen
 ? APPLICANT: Fong, Sherman
 ? APPLICANT: Gao, Wei-Qiang
 ? APPLICANT: Gerber, Hanspeter
 ? APPLICANT: Gerritsen, Mary E.
 ? APPLICANT: Goddard, A.
 ? APPLICANT: Godowski, Paul J.
 ? APPLICANT: Grimaldi, Christopher J.
 ? APPLICANT: Gurney, Austin L.
 ? APPLICANT: Hillan, Kenneth, J.
 ? APPLICANT: Kljavin, Ivar J.
 ? APPLICANT: Mather, Jennie P.
 ? APPLICANT: Pan, James
 ? APPLICANT: Paoni, Nicholas F.
 ? APPLICANT: Roy, Margaret Ann
 ? APPLICANT: Stewart, Timothy A.
 ? APPLICANT: Tumas, Daniel
 ? APPLICANT: Williams, P. Mickey
 ? APPLICANT: Wood, William, I.
 ? TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ? TITLE OF INVENTION: Acids Encoding the Same
 ? FILE REFERENCE: 10466-14
 ? CURRENT APPLICATION NUMBER: US/09/902,775A
 ? CURRENT FILING DATE: 2001-07-10
 ? PRIOR APPLICATION NUMBER: PCT/US00/04414
 ? PRIOR FILING DATE: 2000-02-22
 ? PRIOR APPLICATION NUMBER: US 60/143,048
 ? PRIOR FILING DATE: 1999-07-07
 ? PRIOR APPLICATION NUMBER: US 60/145,698
 ? PRIOR FILING DATE: 1999-07-26
 ? PRIOR APPLICATION NUMBER: US 60/146,222
 ? PRIOR FILING DATE: 1999-07-28
 ? PRIOR APPLICATION NUMBER: PCT/US99/20594
 ? PRIOR FILING DATE: 1999-09-08
 ? PRIOR APPLICATION NUMBER: PCT/US99/20944
 ? PRIOR FILING DATE: 1999-09-13
 ? PRIOR APPLICATION NUMBER: PCT/US99/21090
 ? PRIOR FILING DATE: 1999-09-15
 ? PRIOR APPLICATION NUMBER: PCT/US99/21547
 ? PRIOR FILING DATE: 1999-09-15
 ? PRIOR APPLICATION NUMBER: PCT/US99/23089
 ? PRIOR FILING DATE: 1999-10-05
 ? PRIOR APPLICATION NUMBER: PCT/US99/28214
 ? PRIOR FILING DATE: 1999-11-29
 ? PRIOR APPLICATION NUMBER: PCT/US99/28313
 ? PRIOR FILING DATE: 1999-11-30
 ? PRIOR APPLICATION NUMBER: PCT/US99/28564
 ? PRIOR FILING DATE: 1999-12-02
 ? PRIOR APPLICATION NUMBER: PCT/US99/28565
 ? PRIOR FILING DATE: 1999-12-02
 ? PRIOR APPLICATION NUMBER: PCT/US99/30095
 ? PRIOR FILING DATE: 1999-12-16
 ? PRIOR APPLICATION NUMBER: PCT/US99/30911
 ? PRIOR FILING DATE: 1999-12-20
 ? PRIOR APPLICATION NUMBER: PCT/US99/30999
 ? PRIOR FILING DATE: 1999-12-20
 ? PRIOR APPLICATION NUMBER: PCT/US00/00219

129	AA	CA	CA	AA	TG	CA	C	A	G	A	G	A	G	A	G	T	C	T	T	A	T	T	G	G	A	C	T	G	T	G	C	186																	
	Db																																																
207	CG	GG	GC	CT	CA	CT	C	T	G	T	T	T	C	T	C	A	G	T	G	G	T	T	T	C	A	T	C	A	C	A	G	A	T	C	G	266													
	Qy																																																
186	TG	GA	T	CC	CA	T	C	C	T	A	T	T	C	T	C	A	G	T	G	C	T	G	T	T	C	A	T	C	A	C	A	G	A	T	T	C	G	245											
	Db																																																
267	CA	G	C	T	C	T	C	A	A	-	-	-	T	T	C	G	G	C	A	A	C	T	T	A	C	A	G	C	A	T	A	A	A	T	A	A	G	A	G	C	T	T	C	323					
	Qy																																																
246	CA	T	C	T	T	T	C	A	A	C	C	T	G	T	G	A	T	G	A	A	A	A	G	T	T	C	A	G	T	A	C	C	T	G	A	A	T	T	C	A	C	A	G	A	G	C	T	C	305
	Db																																																
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	Qy																																																
306	CT	G	C	T	A	C	A	A	T	A	T	G	G	A	T	C	A	G	T	T	C	A	G	T	T	T	C	A	T	T	G	A	C	T	G	A	A	T	T	T	365								
	Db																																																
384	T	C	A	A	T	C	A	G	T	T	T	T	T	T	T	C	T	A	C	A	C	A	A	C	T	T	G	A	C	T	T	G	A	C	T	T	G	A	A	A	A	A	A	A	443				
	Qy																																																
366	T	C	A	A	T	C	A	G	T	C	T	T	T	T	T	C	T	A	C	T	G	A	C	A	C	A	C	A	C	A	C	A	C	A	C	A	C	A	C	A	A	A	A	A	425				
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444	T	T	G	C	T	C	A	G	A	C	A	T	G	G	G	G	C	T	C	A	C	T	G	T	G	T	T	A	T	T	C	G	A	C	A	C	A	C	A	C	A	A	A	A	503				
	Qy																																																
426	C	T	G	C	T	C	A	G	C																																								

RESULT 6

US-09-304-920A-376
Sequence 376, Application US/09904920A
Patent No. 6806352
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.

Db 666 CCCAAGGCAAAATTGGAATGATGTAACCTGTTTCTCAATATTATTTTCGGATTGTGAAAT 725
Qy 744 GCCAGAAATAGTCTCAGGACTAAGTGCAA-----GGAAATACAAGGACATGGCTTAC 798
Db 726 GGTAGGAATTAATTCCTTTGAACAAAGGAAATCTCTTTAAGAACAGAGGCGCAACTCAA 785
Qy 799 ATGCATGAAGAAGAACAAAGAGTGAATGTAATAACCAACCAAAATCCAACATAAGAAAAATAT 858
Db 786 ATGTGTAAGAAGGAAGACAGACATGGCCACACCCACCGCCACACGAGAAATTG 845
Qy 859 CTATCAGGCATCAGAGGACTGCACATGTATGTATTACTTGGGACATAAGTAAAAAGA 915
Db 846 TCGCTGTAACCTTCAAAGGACTTCATAAGTATTGTTACTCTGTATACAAATAAAAAATA 902

RESULT 10
US-09-222-575-29/c
; Sequence 29, Application US/09222575
; Patent No. 6387697
; GENERAL INFORMATION:
; APPLICANT: Yuqiu, Jiang
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: Compositions for the Treatment and Diagnosis of Breast Cancer
; TITLE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 210121.470
; CURRENT APPLICATION NUMBER: US/09/222,575
; CURRENT FILING DATE: 1998-12-28
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Human
US-09-222-575-29

Query Match 6.3%; Score 157.8; DB 3; Length 301;
Best Local Similarity 78.4%; Pred. No. 2.2e-31;
Matches 189; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

Qy 534 TTATATTGGACTGACAGACAGGTGGTGGAGGTGAGTGGCAATGGGAGGATGATACACC 593
Db 301 TTTTATTGGACTGTACAGACAGGTGTCAGGGTCAAGTGGCAATGGTGGAGCGGACACC 242
Qy 594 TTTCACAGATCCCTGACCTTCTGGGATCTGGGAGTCTGGGAGCCCAACAATATATATTTTGGTGA 653
Db 241 TTTGACAAAGTCTCTGAGCTTCTGGGATGTAGGGAGCCCAACAACATAGCTACCCCTGA 182
Qy 654 GGACTGTGCCACATAAGGACTCTTCAAACTCCAGGAAGACTGGAATGATAATCCCTG 713
Db 181 GGACTGTGCCACATAGAGACTCTTCAAACTCCAGGAAGACTGGAATGATAATCCCTG 122
Qy 714 TTTCACAGATGACCTTGGATTTGTGAGATGCCAGAAATAAGTCTCAGGACTTAAGTGCA 773
Db 121 TTTCTCAATATTATTTTCGGATTGTAAGTGTAGGAATAAATCCTTTGAACAAAGGAAA 62

Qy 774 A 774
61 A 61

RESULT 11
US-09-389-681-29/c
; Sequence 29, Application US/09389681A
; Patent No. 6518237
; GENERAL INFORMATION:
; APPLICANT: Yuqiu, Jiang
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE

; FILE REFERENCE: 210121.470C3
; CURRENT APPLICATION NUMBER: US/09/389,681A
; CURRENT FILING DATE: 1999-09-02
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-389-681-29

Query Match 6.3%; Score 157.8; DB 4; Length 301;
Best Local Similarity 78.4%; Pred. No. 2.2e-31;
Matches 189; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

Qy 534 TTATATTGGACTGACAGACAGGTGGTGGAGGTGAGTGGCAATGGGAGGATGATACACC 593
Db 301 TTTTATTGGACTGTACAGACAGGTGTCAGGGTCAAGTGGCAATGGTGGAGCGGACACC 242
Qy 594 TTTCACAGATCCCTGACCTTCTGGGATCTGGGAGTCTGGGAGCCCAACAATATATATTTTGGTGA 653
Db 241 TTTGACAAAGTCTCTGAGCTTCTGGGATGTAGGGAGCCCAACAACATAGCTACCCCTGA 182
Qy 654 GGACTGTGCCACATAAGGACTCTTCAAACTCCAGGAAGACTGGAATGATAATCCCTG 713
Db 181 GGACTGTGCCACATAGAGACTCTTCAAACTCCAGGAAGACTGGAATGATAATCCCTG 122
Qy 714 TTTCACAGATGACCTTGGATTTGTGAGATGCCAGAAATAAGTCTCAGGACTTAAGTGCA 773
Db 121 TTTCTCAATATTATTTTCGGATTGTAAGTGTAGGAATAAATCCTTTGAACAAAGGAAA 62

Qy 774 A 774
61 A 61

RESULT 12
US-09-620-405B-29/c
; Sequence 29, Application US/09620405B
; Patent No. 6528054
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C8
; CURRENT APPLICATION NUMBER: US/09/620,405B
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 495
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-620-405B-29

Query Match 6.3%; Score 157.8; DB 4; Length 301;
Best Local Similarity 78.4%; Pred. No. 2.2e-31;
Matches 189; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

Qy 534 TTATATTGGACTGACAGACAGGTGGTGGAGGTGAGTGGCAATGGGAGGATGATACACC 593
Db 301 TTTTATTGGACTGTACAGACAGGTGTCAGGGTCAAGTGGCAATGGTGGAGCGGACACC 242
Qy 594 TTTCACAGATCCCTGACCTTCTGGGATCTGGGAGTCTGGGAGCCCAACAATATATATTTTGGTGA 653
Db 241 TTTGACAAAGTCTCTGAGCTTCTGGGATGTAGGGAGCCCAACAACATAGCTACCCCTGA 182
Qy 654 GGACTGTGCCACATAAGGACTCTTCAAACTCCAGGAAGACTGGAATGATAATCCCTG 713

|||||
Db 181 GGACTGTGCCACCATGAGAGACTCTTCAAAACCCAGGCAAAATTTGGAATGATGTAACCTG 122
Qy 714 TTTCTACAGTATGCTTGGATTGTGAGATGCCAGAAATAGTCTCAGGACTAAGTGCA 773
Db 121 TTTCTCAATTTTTCGGATTGTGAAATGTTAGGATAAATCTTTGAACAAGGAAA 62
Qy 774 A 774
Db 61 A 61

Query Match 6.3%; Score 157.8; DB 4; Length 301;
Best Local Similarity 78.4%; Pred. No. 2.2e-31;
Matches 189; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

US-09-339-338-29/c
; Sequence 29, Application US/09339338A
; Patent No. 6573368
; GENERAL INFORMATION:
; APPLICANT: Yuqiu, Jiang
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.470C2
; CURRENT APPLICATION NUMBER: US/09/339,338A
; CURRENT FILING DATE: 1999-06-23
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-339-338-29

Query Match 6.3%; Score 157.8; DB 4; Length 301;
Best Local Similarity 78.4%; Pred. No. 2.2e-31;
Matches 189; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

Qy 534 TTATATTGGACTGACAGACAGGTGGTGGAGGTCAGTGGCAATGGGAGGATGATACACC 593
Db 301 TTTTATTGGACTGTCAGACCAAGTTTTCGAGGGTCAGTGGCAATGGGAGGATGATACACC 242
Qy 594 TTTCCAGAGTCCCTGACCTTCTGGGATGCTGGGAGGCCCAACAATATAGTTTTGGTGA 653
Db 241 TTTGACAAAGTCTCTGAGCTTCTGGGATGTTAGGGAGGCCCAACAATATAGTTACCTGGA 182
Qy 654 GGACTGTGCCACCATAGGAGACTCTTCAAACTCCAGGAGAACTGGATGATATATCCCTG 713
Db 181 GGACTGTGCCACCATGAGAGACTCTTCAAAACCCAGGCAAAATTTGGAATGATGTAACCTG 122
Qy 714 TTTCTACAGTATGCTTGGATTGTGAGATGCCAGAAATAGTCTCAGGACTAAGTGCA 773
Db 121 TTTCTCAATTTTTCGGATTGTGAAATGTTAGGATAAATCTTTTGAACAAGGAAA 62
Qy 774 A 774
Db 61 A 61

Query Match 6.3%; Score 157.8; DB 4; Length 301;
Best Local Similarity 78.4%; Pred. No. 2.2e-31;
Matches 189; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

US-09-433-826B-29/c
; Sequence 29, Application US/09433826B
; Patent No. 6579973
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.470C4
; CURRENT APPLICATION NUMBER: US/09/433,826B

RESULT 14
US-09-433-826B-29/c
; Sequence 29, Application US/09433826B
; Patent No. 6579973
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.470C4
; CURRENT APPLICATION NUMBER: US/09/433,826B

; CURRENT FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 474
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-433-826B-29

Query Match 6.3%; Score 157.8; DB 4; Length 301;
Best Local Similarity 78.4%; Pred. No. 2.2e-31;
Matches 189; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

Qy 534 TTATATTGGACTGACAGACAGGTGGTGGAGGTCAGTGGCAATGGGAGGATGATACACC 593
Db 301 TTTTATTGGACTGTCAGACCAAGTTTTCGAGGGTCAGTGGCAATGGGAGGATGATACACC 242
Qy 594 TTTCCAGAGTCCCTGACCTTCTGGGATGCTGGGAGGCCCAACAATATAGTTTTGGTGA 653
Db 241 TTTGACAAAGTCTCTGAGCTTCTGGGATGTTAGGGAGGCCCAACAATATAGTTACCTGGA 182
Qy 654 GGACTGTGCCACCATAGGAGACTCTTCAAACTCCAGGAGAACTGGATGATATATCCCTG 713
Db 181 GGACTGTGCCACCATGAGAGACTCTTCAAAACCCAGGCAAAATTTGGAATGATGTAACCTG 122
Qy 714 TTTCTACAGTATGCTTGGATTGTGAGATGCCAGAAATAGTCTCAGGACTAAGTGCA 773
Db 121 TTTCTCAATTTTTCGGATTGTGAAATGTTAGGATAAATCTTTTGAACAAGGAAA 62
Qy 774 A 774
Db 61 A 61

RESULT 15
US-09-604-287A-29/c
; Sequence 29, Application US/09604287A
; Patent No. 6586572
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C7
; CURRENT APPLICATION NUMBER: US/09/604,287A
; CURRENT FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 301
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-604-287A-29

Query Match 6.3%; Score 157.8; DB 4; Length 301;
Best Local Similarity 78.4%; Pred. No. 2.2e-31;
Matches 189; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

Qy 534 TTATATTGGACTGACAGACAGGTGGTGGAGGTCAGTGGCAATGGGAGGATGATACACC 593
Db 301 TTTTATTGGACTGTCAGACCAAGTTTTCGAGGGTCAGTGGCAATGGGAGGATGATACACC 242
Qy 594 TTTCCAGAGTCCCTGACCTTCTGGGATGCTGGGAGGCCCAACAATATAGTTTTGGTGA 653
Db 241 TTTGACAAAGTCTCTGAGCTTCTGGGATGTTAGGGAGGCCCAACAATATAGTTACCTGGA 182
Qy 654 GGACTGTGCCACCATAGGAGACTCTTCAAACTCCAGGAGAACTGGATGATATATCCCTG 713
Db 181 GGACTGTGCCACCATGAGAGACTCTTCAAAACCCAGGCAAAATTTGGAATGATGTAACCTG 122

No.	Score	Match	Length	DB	ID	Description
1	2517	100.0	2517	21	US-10-812-620-1	Sequence 1, Appli
2	456.2	18.1	2143	10	US-09-814-353-21733	Sequence 21733, A
3	441	17.5	968	9	US-09-965-529-40	Sequence 40, Appl
4	441	17.5	968	10	US-09-969-680A-40	Sequence 40, Appl
5	439.4	17.5	997	9	US-09-903-320-376	Sequence 376, App
6	439.4	17.5	997	9	US-09-903-088B-376	Sequence 376, App
7	439.4	17.5	997	9	US-09-905-231A-376	Sequence 376, App

Qy	744	GCAGAAATAAGTCTCTAGGACTAAGTGC	-----GGAATAACAGGACATGGCTTAC	759
Db	726	GGTAGGAATAAATCTCTTTGAA	CAAGGAAAATCTCTTTTAAGAACAGAAAGCCACAACCTCAA	785
Qy	799	ATGCGATGAAGAGAACAGAGCTGAATGT	TAATAACAAACCAAAATCCCAACATAAGAAAATAT	858
Db	786	AUGTGTAAAGAGAGAGAGCAAGAACAT	TGGCCACACCCACGGCCCCACACAGAAATTTG	845
Qy	859	CTATCAGGCATCAGAAAGGACTGCGACAT	GTATGTATTTACTGGGACATAAGTAAAAAGA	915
Db	846	TGCGCTGAACITCAAGAGGACTTCATA	AGTATTTTGTGTACTCTGTATACAAATAAAAAATA	902

RESULT 13

US-09-908-093-376

; Sequence 376, Application US/09908093

; Publication No. US20030017498A1

GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, A.

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth, J.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Mather, Jennie P.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William, I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: 10466-14

; CURRENT APPLICATION NUMBER: US/09/908,093

; CURRENT FILING DATE: 2001-07-17

; PRIOR APPLICATION NUMBER: 09/665,350

; PRIOR FILING DATE: 2000-09-18

; PRIOR APPLICATION NUMBER: PCT/US00/04414

; PRIOR FILING DATE: 2000-02-22

; PRIOR APPLICATION NUMBER: US 60/143,048

; PRIOR FILING DATE: 1999-07-07

; PRIOR APPLICATION NUMBER: US 60/145,698

; PRIOR FILING DATE: 1999-07-26

; PRIOR APPLICATION NUMBER: US 60/146,222

; PRIOR FILING DATE: 1999-07-28

; PRIOR APPLICATION NUMBER: PCT/US99/20594

; PRIOR FILING DATE: 1999-09-08

; PRIOR APPLICATION NUMBER: PCT/US99/20944

; PRIOR FILING DATE: 1999-09-13

; PRIOR APPLICATION NUMBER: PCT/US99/21090

; PRIOR FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: PCT/US99/21547

; PRIOR FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: PCT/US99/23089

; PRIOR FILING DATE: 1999-10-05

; PRIOR APPLICATION NUMBER: PCT/US99/28214

; PRIOR FILING DATE: 1999-11-29

; PRIOR APPLICATION NUMBER: PCT/US99/28313

; PRIOR FILING DATE: 1999-11-30

; PRIOR APPLICATION NUMBER: PCT/US99/28564

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Result No.	Score	Query Match	Length	DB	ID	Description
1	2517	100.0	2517	6	E54035	E54035 Novel C lec
2	2517	100.0	2517	6	BD094039	BD094039 A novel C
3	2489.8	98.9	2517	10	AB024717	AB024717 Mus muscu
C	1857.2	73.8	21092	10	AC124563	AC124563 Mus muscu
5	1558.4	61.9	1606	10	BC003218	BC003218 Mus muscu
6	1173	46.6	222035	2	AC109882	AC109882 Rattus no
7	574.4	22.8	730	10	AY363175	AY363175 Rattus no
8	461.4	18.3	2144	6	CQ717831	CQ717831 Sequence
9	456.6	18.1	246843	2	AC113782	AC113782 Rattus no
10	456.2	18.1	2143	6	CQ414662	CQ414662 Sequence
11	456.2	18.1	2143	9	AB024718	AB024718 Homo sapi
12	441	17.5	927	9	BC000715	BC000715 Homo sapi
13	441	17.5	968	6	AX083498	AX083498 Sequence
14	439.4	17.5	997	6	BD172543	BD172543 Secretd
15	439.4	17.5	997	6	BD172862	BD172862 Secretd
16	439.4	17.5	997	6	BD173181	BD173181 Secretd
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Db		1201	TCTGTGTTCTCCAAACAGTGAAGATGCAATCTTTGAGTCTTTAAACTTTACCTGCGCTT	1260
Qy		1261	GGGAATGGCATGGCCCTTTCAGCAAGGACATCTCCATATGGAAGGCGGCTCAAACTTCA	1320
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Qy		1381	TTCTATAAAGTGGATTTCACTGTATCTACTGCGCAAGTAGAACCTGCTCAGTA	1440
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Qy		1501	TATTCATGATATCTGTCAATATATAGACCATGTTTCTTCCAGACAAAGCCCATAGGAAC	1560
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Qy		1561	TTCAGCAGAGTCAACATTTGTAATAAACAATGATCTCTTGTAGTAGGAATAATTTAAACTAAA	1620
Db		1561	TTCAGCAGAGTCAACATTTGTAATAAACAATGATCTCTTGTAGTAGGAATAATTTAAACTAAA	1620
Qy		1621	TAAATTAATTTGTCAATATTTAGCAGCTTATTCAGGACCTTCTATTTAGACTTTCTCAACATC	1680
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Qy		1801	ATGAACCATCTCTTACTCTCTCACTCAACCTGCTCTCTTCCACTCTCACTGATTTTCCC	1860
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SOURCE Mus sp.
ORGANISM Mus sp.
REFERENCE Akira,S. and Matsumoto,M.
AUTHORS Akira,S. and Matsumoto,M.
TITLE A novel C-type lectin and its genes
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VERSION
KEYWORDS
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1 (sites)
Matsumoto, M., Tanaka, T., Kaisho, T., Sanjo, H., Copeland, N.G.,
Gilbert, D.J., Jenkins, N.A. and Akira, S.
A novel LPS-inducible C-type lectin is a transcriptional target of
NF-IL6 in macrophages
J. Immunol. 163 (9), 5039-5048 (1999)
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PUBMED
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Akira, S. and Matsumoto, M.
Direct Submission
Submitted (09-MAR-1999) Shizuo Akira, Osaka University, Department
of Host Defense, Research Institute for Microbial Diseases; 3-1
Yanada-oka, Suita, Osaka 565-0871, Japan
(E-mail: sakira@biken.osaka-u.ac.jp, Tel:81-6-6879-8303,
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Db 1321 GTTCCTAACAGATTGTGATCTAGTCCACTCTTCTCTGGAGCCCAATTTTCTCTGTGTTCTC 1380
Qy 1381 TTCTATAAACTGGATTTTCACTGTACTGTATCTACTGCGCAAGTAGAACCTGCTCAGTA 1440
Db 1381 TTCTATAAACTGGATTTTCACTGTACTGTATCTACTGCGCAAGTAGAACCTGCTCAGTA 1440
Qy 1441 GGTTCAAAGTGAAATTTATTTAAAAATTCATGTTTCAATTTTCTGTCTCAGGACTGCATT 1500
Db 1441 GGTTCAAAGTGAAATTTATTTAAAAATTCATGTTTCAATTTTCTGTCTCAGGACTGCATT 1500
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Db 1501 TATTGCATGATATTCTGCTCAATATAGACCATGTTTCTTCAGACAAAGCCCTTAAAGGAAC 1560
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Db 1561 TTCAAGCAGCAGTCACACATTTGTAATAAACATGTATCTTGAAGTAGGAAAAATTAACCTAAA 1620
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Db 1621 TAAATTAATTTGTTCATATTAGCCTCATTTAGCAGCCTTCTATTTAGACTTTTCTCACAAATC 1680
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Qy 1741 CTTCCTTTTAAATTTATTTTGTGTAATTTTGTGCAATTTATATATTAATTTACTTTTA 1800
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Qy 2281 AAACCTGAAGTGATCATGATAGATAACTTTTGGATCTTTTCACTTTTCTATTGCTGTGATG 2340
Db 2281 AAACCTGAAGTGATCATGATAGATAACTTTTGGATCTTTTCACTTTTCTATTGCTGTGATG 2340
Qy 2341 AAAATGACCAAAATCTATCTTGGGCGGGAATAATTTTAAATTTATCTTTAAACATAAATTC 2400
Db 2341 AAAATGACCAAAATCTATCTTGGGCGGGAATAATTTTAAATTTATCTTTAAACATAAATTC 2400
Qy 2401 CTATTTAGAAATTTGGAAGGAGGGAATTCATCCAAATTTGAAATTTGAAATTTGAGTGTTC 2460
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QY      2461  TGTACATTAGGTTACAGAAACAACTTTAGCCACAAATAAAGTAATAAACTATT 2517
AC124563/c
LOCUS   AC124563.4          210092 bp      DNA      linear   ROD 25-NOV-2003
DEFINITION Mus musculus BAC clone RP23-206B15 from chromosome 6, complete
sequence.
ACCESSION AC124563
VERSION   AC124563.4   GI:33300796
KEYWORDS  HTG
SOURCE    Mus musculus (house mouse)
ORGANISM  Mus musculus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 210092)
AUTHORS   Abbott,S. and Meyer,R.
TITLE     The sequence of Mus musculus BAC clone RP23-206B15
JOURNAL   Unpublished (2001)
REFERENCE 2 (bases 1 to 210092)
AUTHORS   Wilson,R.
TITLE     Sequencing of Mus musculus
JOURNAL   Unpublished (2001)
REFERENCE 3 (bases 1 to 210092)
AUTHORS   McPherson,J.D. and Waterston,R.H.
TITLE     Direct Submission
JOURNAL   Submitted (14-JUN-2002) Genome Sequencing Center, 4444 Forest Park
          Parkway, St. Louis, MO 63108, USA
REFERENCE 4 (bases 1 to 210092)
AUTHORS   McPherson,J.D. and Waterston,R.H.
TITLE     Direct Submission
JOURNAL   Submitted (15-APR-2003) Genome Sequencing Center, 4444 Forest Park
          Parkway, St. Louis, MO 63108, USA
REFERENCE 5 (bases 1 to 210092)
AUTHORS   Wilson,R.K.
TITLE     Direct Submission
JOURNAL   Submitted (29-JUL-2003) Genome Sequencing Center, 4444 Forest Park
          Parkway, St. Louis, MO 63108, USA
REFERENCE 6 (bases 1 to 210092)
AUTHORS   Wilson,R.
TITLE     Direct Submission
JOURNAL   Submitted (25-NOV-2003) Department of Genetics, Washington
          University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
          On Jul 29, 2003 this sequence version replaced gi:29837778.
          ----- Genome Center
          Center: Washington University Genome Sequencing Center
          Center code: WUGSC
          Web site: http://genome.wustl.edu
          Contact: submission@watson.wustl.edu
          ----- Summary Statistics
          Center project name: M_BA0206B15
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. Wea Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see

http://genome.wustl.edu

SOURCE INFORMATION:

The RPCI-23 BAC Library has been constructed by Kazutoyo Osegawa and Minako Tateno in the laboratory of Pieter de Jong (http://www.chori.org) from female C57BL/6J mouse kidney and/or brain genomic DNA. The clone and detailed information can be obtained from Research Genetics, Inc. (http://www.reagen.com) or Pieter de Jong and coworkers at http://www.chori.org

NEIGHBORING SEQUENCE INFORMATION:

This sequence is the entire insert of the clone.

FEATURES	Source
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unsure	141..191
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repeat_region	2046..2186
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QY	2288	AGTGATCATGATAGATAAATCTTTGGATCTTTTCACTTTTCTATGCTGTGATGAAACATG	2347
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QY	2348	ACCCAAACTACTCTGGCGGGGAAATTTAAATTTATCTTACATAAATTTTCTTATTTA	2407
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QY	2408	GAAATTTGGACAGTGGGGAATCATCCAATTTGAACTCGAAATGTAGTGTGTTGTACAT	2467
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RESULT 5	
BC003218	1606 bp mRNA linear ROD 29-JUN-2004
LOCUS	Mus musculus C-type (calcium dependent, carbohydrate recognition domain) lectin, superfamily member 9, mRNA (cdna clone MGC:5682 IMAGE:3158063), complete cds.
ACCESSION	BC003218
VERSION	BC003218.1 GI:13096843
KEYWORDS	MGC.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 1606)
AUTHORS	Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diachenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Urdino, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullaby, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Faney, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalek, U., Smalish, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.	
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences	
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)	
12477932	
2 (bases 1 to 1606)	
Strausberg, R.	
Direct Submission	
Submitted (20-FEB-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA	
NIH-MGC Project URL: http://mgc.nci.nih.gov	
Contact: MGC help desk	
Email: cgapbs@mail.nih.gov	
Tissue Procurement: Jeffrey Green M.D.	
cDNA Library Preparation: Life Technologies, Inc.	
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)	
DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center	
Center code: BCM-HGSC	
Web site: http://www.hgsc.bcm.tmc.edu/cdna/	
Contact: amg@bcm.tmc.edu	
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Louleaged, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.	
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov	
Series: IRAC Plate: 6 Row: 1 Column: 23	
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 9910161.	
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/clone_lib="NCI CGAP_Mam6"	
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82. .726	
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/codon_start=1	
/product="C-type lectin, superfamily member 9"	
/protein_id="AAH03218.1"	
/db_xref="GI:13096844"	
/db_xref="LocusID:56619"	
/db_xref="MGI:1861232"	
/translation="MNSTKSPASHHTEGCFKNSQVLSWTIAGASILFLSGCFITRCV /translating="KLSKCYSEASGVNCCNWKHYQSCYFSTTILTS VYLRSSQSGNLOPHRIKLSKCYSEASGVNCCNWKHYQSCYFSTTILTS SLLKSCSDMGALHVLVDIQEQLFRTPKPKRKFYIGLTDQVVGQWVDTPETE SLSPWDAGEPNVLVEDCATIRUSSNRKNWDIPCFYSMPWICEMPEISPLD"	
Query Match	61.9%; Score 1558.4; DB 10; Length 1606;
Best Local Similarity	98.9%; Pred. No. 0;

Matches 1579; Conservative		0; Mismatches	16; Indels	1; Gaps	1
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Qy	103	GAAGGCGAGGAAAAAGGAGAAATGAATTCACACCAAAATCGCCTGCATCCCAACACACAGAG	162		
Db	61	GAAGGCGAGGAAAAAGGAGAAATGAATTCACACCAAAATCGCCTGCATCCCAACACACAGAG	120		
Qy	163	AGAGGATGCTTCAAAAACTCCCAAGTGTCTCTCTGGAGCATAGACCGGGGCTCCATCTCG	222		
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Qy	703	GATTAATCCCTGTTTCTACAGTATGCCCTTGGATTTGTGAGATGCCAGAAATAGTCTCTCAG	762		
Db	661	GATTAATCCCTGTTTCTACAGTATGCCCTTGGATTTGTGAGATGCCAGAAATAGTCTCTCAG	720		
Qy	763	GACTAAGTGCAGGAAATACAAGGGACATGCTTTACATGCATGAAGAAGAACCAAGAGTGA	822		
Db	721	GACTAAGTGCAGGAAATACAAGGGACATGCTTTACATGCATGAAGAAGAACCAAGAGTGA	780		
Qy	823	ATGTAATAACCAACCAAAATCCAAACATTAAGAAATATCTATCAGGCATCAGAGGACTGCA	882		
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Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowig, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, X., London, P., Longacre, S., Lopez, J., Lohensuaw, L., Louie, H., Lozano, R.J., Lu, X., Ma, J., Maheshwari, M., Mahindaratne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mawhney, S., McLeod, M.P., McNeill, T.Z., Meenen, E., Milosavljevic, A., Miner, G., Minja, E., Montenayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munitasa, M., Murphy, M., Naif, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwaokemele, O., Okwuonu, G., Olarnpunsagoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L., Puaor, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savary, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Umani, K., Valas, R., Vera, V., Villaseana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wlarczyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, E., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstein, G., and Gibbs, R.A.

TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

Direct Submission
2 (bases 1 to 222035)
Worley, K.C.

Submitted (08-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 222035)

Rat Genome Sequencing Consortium.
Direct Submission
Submitted (11-OCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

COMMENT

On Oct 9, 2002 this sequence version replaced gi:21744187.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GQJU
Center clone name: CH230-310L5
----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 202672 bases at least Q40
Consensus quality: 204982 bases at least Q30
Consensus quality: 206533 bases at least Q20
Estimated insert size: 208212; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 4 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 7987: contig of 7987 bp in length
* 7988 8087: gap of unknown length
* 8088 11519: contig of 3432 bp in length
* 11520 175535: gap of unknown length
* 175536 175535: contig of 163916 bp in length
* 175536 175535: gap of unknown length
* 175536 222035: contig of 46400 bp in length.

FEATURES

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misc_feature
9488..11519
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misc_feature
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/note="wgs contig"
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site:MboI
end_sequence:RXALO63TJ"

ORIGIN

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Best Local Similarity 80.5%; Pred. No. 6.5e-238;
Matches 1557; Conservative 0; Mismatches 335; Indels 43; Gaps 14;
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DB 18755 CCACAGCTTCGGGATGCTGGAGACCCCAATACATAGTTTTGGTGGAGGACTGTGCCAC 18814
QY 666 CATAAGGGACTCTTCAAACTCCAGGAAGAACTGGAAATGATATCCCTGTTCTACAGTAT 725
DB 18815 CATGAGGACTCTTCAAACTCCAGGAAGAACTGGAAATGATATCCCTGTTCTACAGTAT 18874
QY 726 GCCTTGGATTGTGAGATGCCAGAAATAGTCTCAGGACTAAGTCAAGGAATACAG 785
DB 18875 GCCTTGGATTGTGAGATGCCAGAAATAGTCTTGGACTAGGTGCAAGGAACACAGA 18934
QY 786 GGACATGGCTTACATGCAAGAAAGAAACAAAGTGAATGTATAACCAACCAAAATCCAA 845
DB 18935 AGACATGGTTTACATGCAAGAAAGAAACAAAGTGAAGTGAACACACCTAAATCCAA 18994
QY 846 CATAAGAAATATCTATCAGGCATCAGAGGAGCTGCACATGATGATTTACTGGGACATA 905
DB 18995 CACAAGAAATGGCTGTGGGCATCAGAAAGGCCACATATGATGTATTATGAAATA 19054
QY 906 AGTAAAGA-CTTGTTCCCATGCTTAAAGTCCACAGCATTTGTCGTGGTCTTGCCAT 964
DB 19055 AGTAAATGAGTGTGTTTCCATGGCTTAAATCCACAGAAATCATCTGACGTTCTGCCAT 19114
QY 965 AACCTGAAAGATCTCTTTTACAGTGTACAGATCAATCTCTAAACAATGCAACGAAG 1024
DB 19115 AACCTGAAAGTCTCTTTTACAGATATACAAAGCAATCTCTTAATAATGCAAGACA 19174
QY 1025 AAAGGATTCCTCTTTTACATCTCTCTTGGACATCTGCTGCTCATGAG-----A 1076
DB 19175 AAAGGAACTCTCTTTTACATCTCTCTTCCCAAGGAAATGATATGAAGGAGGATA 19234

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ORIGIN	Query Match Best Local Similarity Matches	22.8%; Score 574.4; DB 10; 89.7%; Pred. No. 4.3e-111; Conservative 0; Mismatches 69; Indels 3; Gaps 1;	Length 730;
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QY	165	AGGATGCTTCACAAAACCTCCNAGTGTCTCCTGGAGATAGCGGGGCTCCATCCTGTT 224	
Db	92	AGAACTCTTCACAAAACCTCCNAGTGTCTTCATGGACGATGGCTGGGGCTCCATCCTGTT 151	
QY	225	TCTCAGTGGCTGTTTCATCACACAGATGTGTCTGTAACATATCGCAGCTCTCAAAATTTCCGG 284	
Db	152	TCTCAGTGTCTGTTTCATCACACAGATGTGTGTAACATATCACAGTTTCAAAATTTATGG 211	
QY	285	GC---AGAACTTACAGCCACATAGAAAATTTAAGGAGCTTCTCTGCTACAGTGAGGCATC 341	
Db	212	GCAGAAGAAGTTTACAGCCACATAAAACTATTAAAGGAGCTTCTCTGCTACCTTGAAGCATC 271	
QY	342	AGTTTCAGTCAAGAAATTCCTGCTTGAACCTGGAACATATTATCAATCTAGTTGTTATTT 401	
Db	272	AGTTTCAGTCAAGAAATTCCTGCTTGAACCTGGAACATATTTCAGTCTAGTTGTTACTTT 331	
QY	402	TTTCTCTACGACAACTTGACCTGGTTCATCAAGTTTAAAGAAATTTGCTCAGACATGGGGC 461	
Db	332	TTTCTCTACAACTTATCTGGCTATCAAGTCTAAAGAAATTTGCTCAGACATGGGGC 391	
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QY	522	AAGGAAGATTTTATTTAGGACTGACAGCCAGGTGGTGGGGTTCAGTGGCAATGGGA 581	
Db	452	AAGAAAGATTTTATTTAGGACTGACAGCCAGGTGGTGGGGTTCAGTGGCGATGGGT 511	
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QY	642	AGTTTGGTGGAGACTGTGCCACCATAAAGGACTCTTCAAACTCCAGGAAGAACTGGAA 701	
Db	572	AGTTTGGTGGAGACTGTGCCACCATGAGGACTCTTCAAAACCCAGGAAGAACTGGAA 631	
QY	702	TGATAATCCTGTTTCTACAGTATGCTTGGATTTGTGAGATGCCAGAAATAGTCCTCA 761	
Db	632	TGATGATCCTGTTTCTTACAGTATGCTTGGATTTGTGAGATGCCAGAAATAGTCCTTT 691	
QY	762	GGACTAAGTCAAGGAAAATACAGGAGCATGGCTTACAT 800	
Db	692	GGACTAAGTCAAGGAAACACAGAAACATGGTTTACAT 730	

RESULT 8
CQ717831
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DEFINITION Sequence 3765 from Patent WO02068579.
ACCESSION CQ717831
VERSION CQ717831.1 GI:42278688
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
TITLE Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses

thereof	JOURNAL	Patent: WO 02068579-A 3765 06-SEP-2002;	
	PE Corporation (NY) (US)		
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QY	87	AGAGAAAGAAAGGAGAAAGGAGGAGGATGCTTCAAAAACCTCCCAAGTGTCTCTCGACCATTCGCTGC 146	
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QY	147	ATCCACACACACAGAGAGGATGCTTCAAAAACCTCCCAAGTGTCTCTCGACCATTCG 206	
Db	175	AACACATGCAAGAGAGGATGCTTC---TCCTCCCAATGTTCTTATGAGCTGTTGC 231	
QY	207	CGGGCTCCATCCTGTTTCTCAGTGGCTGTTTCATACACAGATGTGCTGAACATATCG 266	
Db	232	TGGGATCCCATCTCTATTTCTCAGTGCCTGTTTCATACACAGATGTGTTGACATTCG 291	
QY	267	CAGCTCTCAA---TTTCCGGGACACTTACAGCCACATAGAAATATTAGGAGCTTTC 323	
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QY	324	CTGTCTACAGTGAAGGATCAGGTTCAAGTCAAGAAATTCCTTCTTGAATCGAAAAATTA 383	
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QY	384	TCAATCTAGTTGTTATTTTCTCTACGACAACTTGAACCTGTGCTCATCAAGTTTAAAGAA 443	
Db	412	TCAATCCAGCTGCTACTTCTTTCTTCTACGACACCATTTCTCTGGGCGTTAAGTTTAAAGAA 471	
QY	444	TTGCTCAGACATGGGGCTCAGCTGGTGTTCAGACACAGGAGAGGAGGAAATTCCT 503	
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1249 CTGCCAAGCATATATCGTCTTTTACTCCCTGTATATAGTAAAGAGCTTCTTCAAG 1308
Qy ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1239 TCTTTAACTTTACCTCGCGCTGGGAGAAATGGCATGGCCTT-----CAGCAAG 1286
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1309 TCATGAACCTTA-TTCCTGCTCAGAAATACCGGTGTGGCTTCTGGCTACAGGCTCCAC 1367
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1287 GACATCTCCATATGGAAGGCGGTCAAACTTCAGTTCCTTAACAGATTGTGATCTAGTCC 1346
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1368 TGCACCTTCTTAGGAGAGGCGATCGACCATCAGTCCAAACAGGCTGTAAACAAAGTCC 1427
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1488 AGATTTTGTATCTATGCTCAGTAGAGCCGAGTCCAAATAGTCAAT-TTATTTTAAGCG 1546
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1462 AAAATTCATGTTTCACATTTTCTGTCTCAGGAC 1494
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1547 AACATTCATCCACACTTCTCTGTCTCAAGCC 1579

RESULT 9
AC113782
LOCUS
DEFINITION Rattus norvegicus clone CH230-97B16, *** SEQUENCING IN PROGRESS
AC113782
ACCESSION
VERSION HTG; HTGS PHASE1; HTGS DRAFT; HTGS_ENRICHED.
KEYWORDS Rattus norvegicus (Norway rat)
SOURCE
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 246843)
Muzny,D,Marie., Metsker,M, Lee., Abramzon,S., Adams,C., Alder,J.,
Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
Bigswain,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
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Cleveland,C., Cockrell,K., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
Davila,M.B., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
Delgado,O., Denson,S., Detamo,C., Ding,Y., Dinh,H., Divya,K.,
Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K.,
Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,
Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,
Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,W.,
Gebregiorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W.,
Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K.,
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Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S. L., Hodgson, A., Hogue, M., Hollins, B., Howells, S., Hulyk, S., Hume, J., Idiebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpach, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C. L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensuahuwa, L., Loulseghe, H., Lozano, R. J., Lu, X., Ma, J., Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangun, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mawhiney, S., McLeod, M. P., McNeill, T. Z., Meenen, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwakoleneh, O., Okwuonu, G., Olarnpunsagoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L., Puzo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M. A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S. J., Sanders, W., Savary, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sleson, I., Sitter, C. D., Smaje, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Uemami, K., Valas, R., Vera, V., Villalana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausen, A., Weiss, R., Smith, D. R., Holt, R. A., Smith, H. O., Weinstock, G. and Gibbs, R. A.

Unpublished
2 (bases 1 to 246843)
Worley, K. C.
Direct Submission
Submitted (05-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 246843)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (15-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Nov 15, 2002 this sequence version replaced gi:23267207.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GSGL
Center clone name: CH230-97B16
----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 214283 bases at least Q40
Consensus quality: 217684 bases at least Q30
Consensus quality: 220184 bases at least Q20
Estimated insert size: 222530; sum-of-contigs estimation

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Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
* NOTE: Estimated insert size may differ from sequence length
  (see http://www.hgsc.bcm.tmc.edu/docs/Genbank\_draft\_data.html).
* NOTE: This is a 'working draft' sequence. It currently
  consists of 5 contigs. The true order of the pieces
  is not known and their order in this sequence record is
  arbitrary. Gaps between the contigs are represented as
  runs of N, but the exact sizes of the gaps are unknown.
  This record will be updated with the finished sequence
  as soon as it is available and the accession number will
  be preserved.
* 1
* 32891: contig of 32891 bp in length
* 32892
* 32891: gap of unknown length
* 32992
* 241925: contig of 208934 bp in length
* 241926
* 242025: gap of unknown length
* 242026
* 243003: contig of 1278 bp in length
* 243004
* 243003: gap of unknown length
* 243004
* 244504: contig of 1051 bp in length
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* 244554: gap of unknown length
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misc_feature
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misc_feature
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ORIGIN
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Best Local Similarity 71.3%; Pred. No. 28-86;
Matches 580; Conservative 0; Mismatches 224; Indels 9; Gaps 4;

QY 1711 TACAATATATCTTACCAACACACATTTGACTTCTCTTTTAAAAATTAATTTTGTGAA 1770
DB 32890 TTTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 32949

QY 1771 AATTTGTGCATTTATATTAATCTCTTTAATGAACCCATCTTACTCTCTCTACTACAA 1830
DB 32950 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 33009

QY 1831 CTGTCTCTTATCCACTACTGATTTTCCCTCCCAATTTTCATGTCTCTCTCTTTTAA 1890
DB 33010 TCTGCCCTTGCCTCACTGCTTTTCCCTGACAAATTCATGTCTCTTTTGTGTTTA 33069

QY 1891 AACCCACTCTATCTGCTAGTCTTCTCTGAATGCACTTGAGTATAGGCTTTCTACTGGA 1950
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VERSION CQ414662.1 GI:41322443
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
  1.
AUTHORS Lee, J. and Lillie, J.
TITLE Genes, compositions, kits, and method for identification,
  assessment, prevention, and therapy of ovarian cancer
JOURNAL Patent: WO 0170979-A 21733 27-SEP-2001;
  Millennium Pharmaceuticals, Inc. (US)
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AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
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	Yuan, J.		
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JIAN ZHENG,		
PI JEAN YUAN		
PC C12N15/09, C07K14/47, C07K16/18, C07K19/00, C12N1/19, C12N1/21, PC		
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 9, 2005, 02:18:26 ; Search time 1325 Seconds
(without alignments)
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Searched: 4390206 seqs, 2959870567 residues
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	441	17.5	968	4	AAF81743 Human mem
5	441	17.5	976	10	ADF90738 Human hep
6	441	17.5	990	7	ADR41300 Human CD-
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ALIGNMENTS

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XX AC AAF86349;
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KW immune disorder; nuclear factor interleukin 6; NF-IL6; 88.
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XX PN WO200127271-A1.
XX PD 19-APR-2001.
XX PF 02-OCT-2000; 2000WO-JP006820.
XX PR 15-OCT-1999; 99JP-00293724.
XX PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX PI Akira S, Matsumoto M;
XX DR WPI; 2001-273771/28.
XX DR P-PSDB; AAB97225.
XX PT New macrophage activating C-type lectin for the treatment of immune
XX disorders and inflammation.
XX PS Claim 4; Fig 4; 60pp; Japanese.
XX CC This invention relates to a C-type lectin, termed Mincle, which is formed
XX from a transcriptional target gene of nuclear factor interleukin 6 (NF-

Db 592 GGGTCAGTGGCAATGGTGGACGGCACACTTTTGACAAAGTCTCTGAGCTTCTGGGATGT 651
QY 624 TGGGGAGCCCAACAATATATAGTTTGGTGGAGGACTGTGCCACCATATAGGAGACTCTTCAA 683
Db 652 AGGGAGGCCCAACAACATATAGTACCTCGGAGGACTGTGCCACCATATAGGAGACTCTTCAA 711
QY 684 CTCCAGGAAGAACTGGAATGATAATCCCTGTTTCTACAGTATGCGCTTGGATTGTGAGAT 743
Db 712 CCCAAGGCAAAATTGGAATGATGTAACTTCTTCCCAATATTTTCGGATTGTGGAAT 771
QY 744 GCCAGAAATTAAGTCTCCAGGACTTAAGTGCAA-----GGAAATACAGGAGACATGGCTTAC 798
Db 772 GGTAGGAATAAATCTTTTGACAAAGGAAATCTCTTTAAGAACAGAGGACCAACTCAA 831
QY 799 ATGCATGAAGAGAACAGAGTGAATGTAATACAAACCAAAATCCAACTATAGAAATAT 858
Db 832 ATGTGTAAGAAGAGAGCAAGAACATGGCCACACCCGCCCCACACGAGAAATTTG 891
QY 859 CTATCAGGCATCAGAGGAGCTGCACATGTATGTATTACTGGGACATAGTAAGTAAGACTT 918
Db 892 TGGGCTGAACCTTCAAAGGACTTCTAAGTATTTTGTACTCTGATATAAATAAATAAGT 951
QY 919 GTTCCCAATTGCTAAAAGTCCACAGCATTTGTCTGATGG-----TCTTGCCATTAACCTG 970
Db 952 AGTTTTAAATGTATTAATTCATGTTTACTGGCTGAAGTGCAATTTCTCTCTAGCTTAGTCT 1011
QY 971 AAAGATCTCTTTTACAGTGTACAGATCAATTTCTTAACAATGCAACAGAAAGAGG 1030
Db 1012 CAGGTCTCTTCCAGAAATTTTACAAAGCAATTCATACCTTTTGTCTACATTTGCGCTCATTT 1071
QY 1031 ATTCTCTCTTTTACATCTGTCTTGACATCTGTCTTGCTCATGAGAAATGATATGAAGA 1090
Db 1072 TTTAGTGTTCGATGAAGATACAGGACACGGAGCCAGACAGAGTCTAGCAAGAGG 1131
QY 1091 AGAGGTAGAAAGCAGATGTCTGTATTAAGAGACTTTTAATGGTCACATATGTCATCTCTGTT 1150
Db 1132 GATTTTGAAGTGCCTTCCAAAATCTCTGAATCCGGCTCTGTAGCAGGTCTCTTTC 1191
QY 1151 TTTCTACATCTTGGCTCTAGCTTATCTATCTATCAGTACATAGATCACTTCTGTGTTCT 1210
Db 1192 TTTCTAGCTTCTGACAAGTCTGTCTTCTCTCTTGTGTTTTCATACCGTCTTCTATCTCTG 1251
QY 1211 CCA-----ACAGTGAGGAGATGATCATCTTTGAGTCTT 1242
Db 1252 CCAAGCATATATGCTCTTTTACTCCCTGTATATGATGAAGAGCTTCTTCAAGTCA 1311
QY 1243 TAAACTTACCTGCGCTTGGGAGAAATGGCATGGCTT-----CAGCAAGGACA 1290
Db 1312 GAAACTTA--TTCTGCTCAGATACCGGTGTGGCTTTCTGGCTACAGGCTCCACTGCA 1370
QY 1291 TCTCATATGGAAGCCCGGTCAAACTTCAGTTCTCTAAAGATGTGATGTAGTCCACTC 1350
Db 1371 CTTCTTTAGGAAGGCGATGCCAGCCATCAGCTCCAAACAGGCTGTAAACAAAGTCCACCC 1430
QY 1351 -TTCCGTGAGCCCAATTTCTGTGTTCTCTCTATAAC---TGGATTTCACTGTA 1405
Db 1431 ATCCCTGGGGCTTCTTGTCTGCTTATTTTCAATTTGACTGAATGGATCTCACCAGAT 1490
QY 1406 CTGTGATCTACTCGCAAGTAGAACCTGTCTCAGTAGGTTCAAAGTGAATTTTAAATAA 1465
Db 1491 TTTGTATCTATTGCTCAGCTAGAGACCCGAGTCAATAGTCAATTT-ATTCTAAGCGAAC 1549
QY 1466 TTCAATGTCACATTTTCTGTCTCAGGAC 1494
Db 1550 TTCAATGTCACATTTTCTGTCTCAGGAC 1578

RESULT 3
ADO24494
ID ADO24494 standard; cDNA; 2143 BP.
XX
AC ADO24494;

XX 12-AUG-2004 (first entry)
DT Human PRO244 encoding cDNA SEQ ID NO:133.
XX human; PRO; antianaemic; antiarthritic; antiinflammatory; antipsoriatic;
DE antirheumatic; dermatological; immunostimulant; immunosuppressive;
XX osteopathic; vasotropic; immune related disease;
KW inflammatory immune response; rheumatoid arthritis; osteoarthritis;
KW juvenile chronic arthritis; systemic lupus erythematosus;
KW spondyloarthritis; systemic sclerosis;
KW idiopathic inflammatory myopathy; Sjogren's syndrome;
KW systemic vasculitis; sarcoidosis; autoimmune haemolytic anaemia;
KW autoimmune disease; immune-mediated skin disease; bullous skin disease;
KW erythema multiforme; contact dermatitis; psoriasis; lymphadenopathy;
KW splenomegaly; leukopenia; gene; ss.
XX Homo sapiens.
XX WO2004043397-A2.
XX 27-MAY-2004.
XX 12-NOV-2003; 2003WO-US036002.
XX 12-NOV-2002; 2002US-0425931P.
XX (GETH) GENENTECH INC.
XX Abbas A, Bodary S, Clark H, Wu TD, Schoenfeld J, Wood WI;
PI WPI; 2004-420080/39.
XX P-PSDB; ADO24495.
XX New isolated PRO polypeptide e.g. PRO37544, PRO69493, PRO87327 etc,
PT capable of stimulating an immune response, useful for treating diseases
PT such as rheumatoid arthritis, psoriasis, and leukopenia.
XX Claim 2; SEQ ID NO 133; 326pp; English.
XX The present invention describes an isolated human PRO polypeptide (I).
CC Also described: (1) an isolated PRO nucleic (II) acid encoding (I); (2) a
CC vector (III) comprising (II); (3) a host cell (IV) comprising (III); (4)
CC producing (I); (5) a chimeric molecule (V) comprising (I) fused to a
CC heterologous amino acid sequence; (6) an antibody (VI) which specifically
CC binds to (I); (7) a composition of matter comprising (I), an agonist of
CC (I), an antagonist of (I), or (VI) in combination with a carrier; (8)
CC treating (M1) an immune related disorder in a mammal, by administering
CC (I), an agonist of (I), an antagonist of (I), or the antibody (VI); (9)
CC diagnosing an immune related disease in a mammal, by detecting the level
CC of expression of a gene encoding (I) in a test sample of tissue cells
CC obtained from the mammal and in a control sample of known normal tissue
CC cells of the same cell type; (10) identifying a compound that inhibits
CC the activity of (I); (11) identifying a compound (M2) that inhibits the
CC expression of a gene encoding (I); (12) identifying a compound that
CC mimics the activity of (I); and (12) stimulating the immune response in a
CC mammal, by administering (I) or its antagonist to the mammal. (I) has
CC antianaemic, antiarthritic, antiinflammatory, antipsoriatic,
CC osteopathic and vasotropic activities. (I) and (VI) are useful for
CC diagnosing an immune related disease in a mammal. (II) is useful for
CC diagnosing an inflammatory immune response in a mammal. (VI) is useful
CC for determining the presence of (I) in a sample suspected of containing
CC the polypeptide. (M1) is useful for treating mammal having an immune
CC related disorder chosen from rheumatoid arthritis, osteoarthritis,
CC juvenile chronic arthritis, systemic lupus erythematosus,
CC spondyloarthritis, systemic sclerosis, idiopathic inflammatory
CC myopathies, Sjogren's syndrome, systemic vasculitis, sarcoidosis,
CC autoimmune haemolytic anaemia, autoimmune or immune-mediated skin
CC diseases including bullous skin diseases, erythema multiforme and contact
CC dermatitis, psoriasis, lymphadenopathy, splenomegaly and leukopenia. the
XX present sequence encodes a human PRO protein from the present invention.
XX

Db 606 AGGGAGGCCCAACAATAGCTACCCCTGGAGGACTGTGCCACCATGAGAGACTCTTCAA 665
Qy 684 CTCAGGAAGAACTGGAATGTAATCCCTGTTTCTACAGTATGCCCTTGGATTTGTGAGAT 743
Db 666 CCCAAGGCCAAAATTGGAATGATGTAACCTGTTTCTCCTCAATTTTCGGATTTGTGAAT 725
Qy 744 GCAGAAATAAGTCTCTCAGGACTTAAGTGCAA----GGAAATACAAGGACATGGCTTAC 798
Db 726 GGTAGAATAAATCTTTTGAACAAGGAAAATCTCTTTAAGAACAGAGGCACAATCAA 785
Qy 799 ATGTCATGAAGAAGAACAAGAGTGAATGTAATAACCAACCAAAATCCAACTAAGAAAATAT 858
Db 786 ATGTGTAAAGGAAGCAAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 845
Qy 859 CTATCAGGCATCAGAAAGGACTGACATGATGATGATGATGATGATGATGATGATGATGATGAT 915
Db 846 TCGCTGAACTTCAAAGGACTTCAATAGTATTTGTTACTCTGTATACAAATAAAAAATA 902

RESULT 11

ID ACA60316 standard; cDNA; 997 BP.

AC ACA60316;

DT 12-JUN-2003 (first entry)

DE Human cDNA for secreted/transmembrane protein PRO244.

KW Human; ss; gene; secreted protein; transmembrane protein; PRO;
KW gene therapy; chromosome identification; chromosome marker.

XX Homo sapiens.

XX US2003003530-A1.

XX 02-JAN-2003.

PF 11-JUL-2001; 2001US-00904011.

PR 17-SEP-1997; 97US-0059113P.
PR 17-SEP-1997; 97US-0059113P.
PR 17-SEP-1997; 97US-0059117P.
PR 17-SEP-1997; 97US-0059119P.
PR 17-SEP-1997; 97US-0059121P.
PR 17-SEP-1997; 97US-0059122P.
PR 17-SEP-1997; 97US-0059184P.
PR 18-SEP-1997; 97US-0059263P.
PR 15-OCT-1997; 97US-0059266P.
PR 17-OCT-1997; 97US-0062125P.
PR 17-OCT-1997; 97US-0062285P.
PR 17-OCT-1997; 97US-0062287P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0062814P.
PR 24-OCT-1997; 97US-0062816P.
PR 24-OCT-1997; 97US-0063045P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
PR 24-OCT-1997; 97US-0063127P.
PR 24-OCT-1997; 97US-0063128P.
PR 27-OCT-1997; 97US-0063327P.
PR 27-OCT-1997; 97US-0063329P.
PR 28-OCT-1997; 97US-0063341P.
PR 28-OCT-1997; 97US-0063342P.
PR 28-OCT-1997; 97US-0063544P.
PR 28-OCT-1997; 97US-0063549P.
PR 28-OCT-1997; 97US-0063550P.
PR 28-OCT-1997; 97US-0063564P.
PR 29-OCT-1997; 97US-0063435P.
PR 29-OCT-1997; 97US-0063704P.
PR 29-OCT-1997; 97US-0063732P.
PR 29-OCT-1997; 97US-0063734P.

PR 29-OCT-1997; 97US-0063735P.
PR 29-OCT-1997; 97US-0063738P.
PR 29-OCT-1997; 97US-0064215P.
PR 31-OCT-1997; 97US-0063870P.
PR 31-OCT-1997; 97US-0064103P.
PR 03-NOV-1997; 97US-0064248P.
PR 07-NOV-1997; 97US-0064809P.
PR 12-NOV-1997; 97US-0065186P.
PR 17-NOV-1997; 97US-0065846P.
PR 18-NOV-1997; 97US-0065693P.
PR 21-NOV-1997; 97US-0066120P.
PR 21-NOV-1997; 97US-0066364P.
PR 24-NOV-1997; 97US-0066453P.
PR 24-NOV-1997; 97US-0066466P.
PR 24-NOV-1997; 97US-0066511P.
PR 24-NOV-1997; 97US-0066770P.
PR 24-NOV-1997; 97US-0066772P.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98WO-US019177.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 01-DEC-1998; 98WO-US025108.
PR 08-SEP-1999; 99WO-US020594.
PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 11-FEB-2000; 2000WO-US000219.
PR 22-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 02-JUN-2000; 2000WO-US014042.
PR 28-JUL-2000; 2000WO-US015264.
PR 24-AUG-2000; 2000WO-US020710.
PR 18-SEP-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00665350.

(GETH) GENENTECH INC.

PI Ashkenazi A, Botstein D, Deenoyers L, Eaton DL, Ferrara N;
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin LJ;
PI Mathier JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PI Williams PM, Wood WI;

WPI: 2003-329602/31.
P-PSDB; ABU71950.

New transmembrane polypeptides and nucleic acids encoding the
polypeptides, useful in gene therapy, in chromosome identification, as
chromosome markers, in generating probes and in tissue typing.

Claim 2; Fig 121; 484pp; English.

The invention relates to an isolated nucleic acid with at least 80%
nucleic acid sequence identity to a nucleotide sequence encoding one of
61 secreted/transmembrane polypeptides, or PRO polypeptides or encoding a
PRO protein extracellular domain. Also included are a vector comprising
the PRO nucleic acid, a host cell comprising the vector, producing a PRO
polypeptide (by culturing the host cell for the expression of the PRO
polypeptide, and recovering the PRO polypeptide from the cell culture),
an isolated PRO polypeptide (having at least 80% sequence identity to: (


```
Db      69  AGAGAGAGAGAAACAAAACCAAGAGAGAGAAAAAATGAATTCATCTAAATCATCTGA 128
Qy      147  ATCCACACACACAGAGAGAGGATGTTCCAAAACCTCCCAAGTGTCTCTCTGGAGGATAGC 206
Db      129  AACACAATGCACAGAGAGAGAGATGCTTC--TCTTCCCAATGTTCTTATGGACTGTTC 185
Qy      207  CGGGCCCTCCATCTCTGTTTCTCAGTGGCTGTTTCAATCAACAGATGTGCTGTAACATATCG 266
Db      186  TGGGATCCCATCTCTATTTCTCAGTGGCTGTTTCAATCAACAGATGTGTTGACATTTTCG 245
Qy      267  CAGCTCTCAAA--TTTCCGGCAGACCTTACAGCCACATAGAAATATTAAGGAGCTTTC 323
Db      246  CATCTTTCAAACTGTGATGAGAAAAAGTTTCAGCTACCTGAGAAATTCACAGAGCTCTC 305
Qy      324  CTGCTACAGTGAAGGATCAGGTTTCAGTCAAGAAATGCTGTCTTGAACCTGGAACATTA 383
Db      306  CTGCTACAAATATGATCAGGTTTCAGTCAAGAAATGTTGTCATTCAGTGAATATTT 365
Qy      384  TCAATCTAGTTGTTATTTTCTCTACGACAACTTGACCTGGTCACTCAAGTTTAAAGAA 443
Db      366  TCAATCCAGCTGCTACTCTTTCTTACTGACACACATTTCTCTGGGCGTTAAGTTTAAAGAA 425
Qy      444  TTGCTCAGACATGGGGCTCACCTGGTGTATTCGACACAGGAGGAGGAGGATTCCT 503
Db      426  CTGCTCAGCCATGGGGCTCACCTGGTGTATTCAGCTCAGGAGGAGGAGGAGGATTCCT 485
Qy      504  TTTTCGACAAAATCTTAAAGGAAAGAGTTTATATGAGCTGACAGACACAGGAGGAGGAGG 563
Db      486  TTCCTACAGAAACCTAAATGAGAGAGTTTATTTGAGCTGTGACACAGGAGGAGGAGG 545
Qy      564  GGGTCAGTGGCAATGGGAGGATGATACACCTTTTCAAGAGTCCCTGACCTTCTGGGATGC 623
Db      546  GGGTCAGTGGCAATGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 605
Qy      624  TGGGAGGCCAACAAATATAGTTTGGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 683
Db      606  AGGGAGGCCAACAAATATAGTTTGGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 665
Qy      684  CTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 743
Db      666  CCCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 725
Qy      744  GCCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 798
Db      726  GGTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 785
Qy      799  ATGATGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 858
Db      786  ATGATGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 845
Qy      859  CTATCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 915
Db      846  TGGCTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 902

RESULT 13
ID ACA73396 standard; cDNA; 997 BP.
AC
XX
XX ACA73396;
XX
DT 01-JUL-2003 (first entry)
XX
DE Human secreted/transmembrane protein (PRO) cDNA #12.
XX
KW Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;
KW proliferation; differentiation; chondrocyte cells;
KW tumour necrosis factor-alpha; TNF-alpha; blood; gene therapy.
XX
OS Homo sapiens.
XX
XX
XX US2003036146-A1.
```

(GETH) GENENTECH INC.


```
Qy 444 TTGCTCAGACATGGGGGCTCACCTGGTGGTTATCGACACACAGGAAGAGCAGGAATTCCT 503
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
426 CTGCTCAGCCATGGGGGCTCACCTGGTGGTTATCAACTCAGAGGAGGACAGGAATTCCT 485
Qy 504 TTTTCGCACAAATCTAAAGGAAGAGCTTTATATTCGACTGCAGACCCAGGTGGTGA 563
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
486 TTCCTACAAGAAACCTAAATAGAGAGTTTTTATTCGACTGTGACACCCAGGTGTGCA 545
Qy 564 GGGTCAGTGGCAATGGGAGGATGATACACCTTTTCACAGAGTCCCTGACCTTCTGGGATGC 623
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
546 GGGTCAGTGGCAATGGGTGGACGGCACACCTTTGACAAAGTCTCTGAGCTTCTGGGATGT 605
Qy 624 TGGGAGCCCAACAATATAGTTTTGGTGGAGGACTGTGCCACCAATAAGGACTCTTCAA 683
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
606 AGGGAGCCCAACAACATAGCTACCCCTGGAGGACTGTGCCACCACTGAGAGACTCTTCAA 665
Qy 684 CTCGAGGAAGAACTGGATGATTAATCCCTGTTTCTACAGTATGCCCTTGGNTTGTGAGAT 743
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
666 CCCAAGGCAAAATTGGAATGATGAACCTGTTTCTCAATTATTTTCGGNTTGTGAAAT 725
Qy 744 GCCAGAAATAAGTCTCAGGACTAAGTGCAA-----GGAAATACAAAGGACATGGCTTAC 798
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
726 GGTAGGATTAATCCTTTGACAAAGGAATCTCTTTAAGAACAGAGGCACAACTCAA 785
Qy 799 ATGCATGAAGAAGAACAAAGATGAATGTAATAACAACCAAAATCCAAATAGGAAATAT 858
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
786 ATGTAAAGAAGGAAGCAAGCAATGGCCACACCCCGCCCAACGAGAAATTTG 845
Qy 859 CTATCAGGCATCAGAGGACTGCACATGTATGTTACTTGGGACATAGTAAAGA 915
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
846 TGCCTGAACCTCAAGGACTTCATAGTATTTGTTACTCTGATACAAATAAATA 902
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Search completed: June 9, 2005, 04:23:54
Job time : 1337 secs

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OM nucleic - nucleic search, using sw model

Run on: June 9, 2005, 03:48:21 ; Search time 8065 Seconds
(without alignments)
11879.450 Million cell updates/sec

Title: US-10-812-620-1

Perfect score: 2517
Sequence: 1 cggctgttactcttgact.....aaataagtaataaatt 2517

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST.*

1: gb_est1.*
2: gb_est2.*
3: gb_hic.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_gsa1.*
9: gb_gsa2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1991	79.1	2233	3 AK089286	AK089286 Mus muscu
2	1338	53.2	4017	3 AK036493	AK036493 Mus muscu
3	818.6	32.5	865	9 BX963867	BX963867 Reverse a
C 4	706.2	28.1	731	4 BG067349	BG067349 H3053D08-
5	696.6	27.7	756	6 BY761232	BY761232 BY761232
6	665.6	26.4	705	6 BY764212	BY764212 BY764212
7	655.2	26.0	701	6 BY763813	BY763813 BY763813
8	650.8	25.9	717	6 BY743963	BY743963 BY743963
9	650.4	25.8	679	9 CR071785	CR071785 Reverse a
10	643.2	25.6	674	6 BY744630	BY744630 BY744630
11	637.8	25.3	666	6 BY747821	BY747821 BY747821
12	635.6	25.3	655	6 BY749084	BY749084 BY749084
13	628.2	25.0	644	4 BG080418	BG080418 H3053D08-
14	625.4	24.8	645	6 BY743467	BY743467 BY743467
15	623.4	24.8	643	6 BY743813	BY743813 BY743813
C 16	615.6	24.5	731	2 BE292591	BE292591 601057892
17	602	23.9	667	6 BY747840	BY747840 BY747840
18	594	23.6	660	2 BE292395	BE292395 601057892
19	581.2	23.1	728	6 BY742764	BY742764 BY742764
20	530.2	21.1	647	6 BY763796	BY763796 BY763796
C 21	528	21.0	548	7 CK329780	CK329780 H8185B09-
22	497.6	19.8	671	6 BY749488	BY749488 BY749488
C 23	484.8	19.3	570	5 BP771395	BP771395 BP771395
24	484.4	19.2	486	5 BX516799	BX516799 BX516799

25	484	19.2	493	6	BY552058	BY552058
26	460	18.3	473	2	BB860060	BB860060
27	456.4	18.1	489	6	BY529779	BY529779
28	440.4	17.5	452	6	BY556050	BY556050
29	439.8	17.5	473	6	BY559970	BY559970
C 30	437.8	17.4	496	6	C86253	C86253
31	434.6	17.3	453	2	BB785184	BB785184
32	433.2	17.2	442	6	BY542553	BY542553
33	432	17.2	452	6	BY552321	BY552321
34	430.2	17.1	436	6	BY544721	BY544721
35	429.8	17.1	441	6	BY563518	BY563518
36	424.6	16.9	454	6	BY535249	BY535249
37	423	16.8	455	6	BY548579	BY548579
38	422	16.8	458	6	BY548502	BY548502
39	421.6	16.8	447	6	BY562107	BY562107
40	421	16.7	464	6	BY598937	BY598937
41	416	16.5	448	6	BY530505	BY530505
42	415.4	16.5	438	6	BY537115	BY537115
43	411	16.3	414	5	BY207927	BY207927
44	409.6	16.3	428	6	BY544585	BY544585
45	409	16.2	429	6	BY539169	BY539169

ALIGNMENTS

RESULT 1	AK089286	2233 bp	mrna	linear	HTC 03-APR-2004
LOCUS	AK089286				
DEFINITION	Mus musculus B6-derived CD11 +ve dendritic cells cDNA, RIKEN full-length enriched library, clone:F730001C01 product:C-type (calcium dependent, carbohydrate recognition domain) lectin, superfamily member 9, full insert sequence.				
ACCESSION	AK089286				
VERSION	AK089286.1	GI:26105181			
KEYWORDS	HTC; CAP trapper.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	Carninci, P. and Hayashizaki, Y.				
TITLE	High-efficiency full-length cDNA cloning				
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)				
MEDLINE	99279253				
PUBMED	10349636				
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AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, Y., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)				
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)				
MEDLINE	20530913				
PUBMED	11076861				
REFERENCE	The RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium. Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)				
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium				
TITLE	Functional annotation of a full-length mouse cDNA collection				
JOURNAL	Nature 409, 685-690 (2001)				
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L.,		
Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y.,		
Rogers,J. and Bradley,A.		
Direct Submission		
Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,		
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Matches 693; Conservative 0; Mismatches 10; Indels 2; Gaps 2;

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ACCESSION BY763813

VERSION BY763813.1

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

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1 (bases 1 to 701) Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,

Nikaido, I., Otsu, N., Saito, R., Suzuki, H., Yamanaka, I.,

Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,

Schönbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C.,

Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,

Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V.,
Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A.,
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Rogers, J., Birney, E. and Hayashizaki, Y.

Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

JOURNAL 22354683

MEDLINE 12466851

PUBMED 12466851

COMMENT

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Adachi, S., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P.,

Fukuda, J., Hashizume, W., Hayashida, K., Hirozane, T., Hori, F.,

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Takeda, Y., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y.

Direct Submission

Computational Analysis of Full-Length Mouse cDNAs Compared with

Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new

genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format

sequencing pipeline with 384 multicapillary sequencer. Genome Res.

10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA

encyclopedia: real-time sequence clustering for construction of a

nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

cDNA library was prepared and sequenced in Mouse Genome

Encyclopedia Project of Genome Exploration Research Group in Riken

Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to

prepare mouse tissues.

Tissues were provided by Dr. John Todd (Dept. of Medical Genetics

Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome

Trust/MRC building Addenbrookes Hospital Cambridge) whose

assistance we gratefully acknowledge.

Please visit our web site (http://genome.gsc.riken.go.jp) for

further details.

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DEFINITION musculus cDNA clone I830025C13 5', mRNA sequence.
ACCESSION BY743963
VERSION BY743963.1 GI:27170313
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

22354683

12466851

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Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hashizume, W., Hayashida, K., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Osato, N., Saito, R., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Takeda, Y., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y.

Direct Submission

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RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Tissues were provided by David A. Hume (Dept. of Biochemistry and Microbiology/Parasitology Institute for Molecular Bioscience University of Queensland Brisbane, Q 4072 Australia) whose assistance we gratefully acknowledge.

Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

/clone="I830025C13"
/tissue_type="bone marrow"
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Matches 677; Conservative 0; Mismatches 9; Indels 2; Gaps 2;

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VERSION
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KEYWORDS
GSS; genome survey sequence; MICER.
SOURCE
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ORGANISM
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 679)

AUTHORS
Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L., Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y., Rogers,J. and Bradley,A.
TITLE
Direct Submission
JOURNAL
Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. http://www.sanger.ac.uk/MICER
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Matches 665; Conservative 0; Mismatches 7; Indels 1; Gaps 1;

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LOCUS BY747821 666 bp mRNA linear EST 17-DEC-2002
 DEFINITION BY747821 RIKEN full-length enriched, NOD-derived CD11c +ve dendritic cells Mus musculus cDNA clone F630011J05 5', mRNA sequence.

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 VERSION BY747821.1 GI:27176312
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 666)
 AUTHORS Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Oeato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batolov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Guscinich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Perte, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Santelina, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, K., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wynehaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Shikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
 JOURNAL Nature 420, 563-573 (2002)
 MEDLINE 22354683
 PubMed 12466851
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 Fax: 81-45-503-9216
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 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hashizume, W., Hayashida, K., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Saito, R., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Takeda, Y., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y.
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 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken

Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
 Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC Building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.
 Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

FEATURES
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 Best Local Similarity 98.3%; Pred. No. 1.1e-143;
 Matches 653; Conservative 0; Mismatches 10; Indels 1; Gaps 1;
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 BY749084 RIKEN full-length enriched, NOD-derived CD11c +ve dendritic cells Mus musculus cDNA clone F630224E05 5', mRNA sequence.
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Mus musculus (house mouse)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 655)
 Okazaki, Y., Furuno, N., Saikawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Otsu, N., Sato, R., Suzuki, H., Yamana, K., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Sult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.P., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Glisi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawai, H., Kawasawa, Y., Kedzierzki, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Akawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shingawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.
 Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)
 22354683
 PUBLISHED
 12466851
 COMMENT
 Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/
 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hashizume, W., Hayashida, K., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Oheato, N., Saito, R., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Takeda, Y., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y.
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 tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.
 Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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 ORIGIN
 Query Match 25.3%; Score 635.6; DB 6; Length 655;
 Best Local Similarity 99.1%; Pred. No. 3.7e-143;
 Matches 649; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
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Sandelin, A., Schneider, C., Semples, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Walestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yaginuma, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayashizaki, N., Hirozane-Kitahara, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E., and Hayashizaki, Y.

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Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hashizume, W., Hayashida, K., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y., Konno, S., Konno, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Saito, R., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Takeda, Y., Waki, K., Watahiki, A., Muramatsu, M., and Hayashizaki, Y.

Direct Submission

Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system - 384-Format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in RIKEN Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Tissues were provided by David A. Hume (Depts. of Biochemistry and Microbiology/Parasitology Institute for Molecular Bioscience University of Queensland Brisbane, Q 4072 Australia) whose assistance we gratefully acknowledge.

Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

Location/Qualifiers

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TITLE

JOURNAL
MEDLINE
PUBMED
COMMENT

ORIGIN

Query Match 24.8%; Score 625.4; DB 6; Length 645;
Best Local Similarity 98.9%; Pred. No. 1.1e-140;
Matches 629; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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BY743813

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,

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Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,

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Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,

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Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M.,

Sandelin, A., Schneider, C., Semples, C.A., Setou, M., Shimada, K.,

Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L. G., Wynehaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S., Rogers, J., Birney, E. and Hayashizaki, Y.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
22354683
PUBMED
12456851
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gscc.riken.jp, URL: http://genome.gsc.riken.jp/
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hashizume, W., Hayashida, K., Hirozane, T., Hori, P., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Nunazaki, R., Ohno, M., Ohsato, N., Saito, R., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Takeda, Y., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y.
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Tissues were provided by David A. Hume (Depts. of Biochemistry and Microbiology/Parasitology Institute for Molecular Bioscience University of Queensland Brisbane, Q 4072 Australia) whose assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

FEATURES

Location/Qualifiers
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ORIGIN

Query Match 24.8%; Score 623.4; DB 6; Length 643;
Best Local Similarity 98.6%; Pred. No. 3.4e-140;
Matches 627; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 2 GGCTGTGTTACTTTGAACCTTTTAAAGAGGGGCAAGGATTCACCATTCAGACTCATT 61
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Search completed: June 9, 2005, 09:38:50
Job time : 8079 secs


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; SEQ ID NO 376
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; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-907-794A-376

Alignment Scores:
Pred. No.: 7,27e-88 Length: 997
Score: 774.00 Matches: 143
Percent Similarity: 79.07% Conservative: 27
Best Local Similarity: 66.51% Mismatches: 43
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US-10-812-620-2 (1-214) x US-09-907-794A-376 (1-997)

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QY 180 AlaThrIleArgAspSerSerAsnSerArgLysAsnTrpAsnAspIleProCysPheTyr 199
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RESULT 2
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; Sequence 376, Application US/09905125A
; Patent No. 6664376
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,125A
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;; PRIOR FILING DATE: 2000-01-05
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;; SEQ ID NO 376
;; LENGTH: 997
;; TYPE: DNA
;; ORGANISM: Homo Sapien
US-09-905-125A-376

Alignment Scores:
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Score: 774.00 Matches: 143
Percent Similarity: 79.07% Conservative: 27
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US-10-812-620-2 (1-214) x US-09-905-125A-376 (1-997)

Qy 1 MetAenSerThrLysSerProAlaSerHisThrGluArgGlyCysPheLysAsnSer 20
Db 106 ATGAATTCATCATTAATCATCTGAAACACAAATGCACAGAGAGATGCTTC---TCCTCC 162
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RESULT 3

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;; GENERAL INFORMATION:
;; APPLICANT: Genentech, Inc.
;; APPLICANT: Ashkenazi, Avi
;; APPLICANT: Botstein, David
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Eaton, Dan L.
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Filvaroff, Ellen
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;; APPLICANT: Roy, Margaret Ann
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;; APPLICANT: Tumas, Daniel
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William, I.
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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;; PRIOR FILING DATE: 1999-11-29
;; PRIOR APPLICATION NUMBER: PCT/US99/28313
;; PRIOR FILING DATE: 1999-11-30
;; PRIOR APPLICATION NUMBER: PCT/US99/28564
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/28565
;; PRIOR FILING DATE: 1999-12-02
;; PRIOR APPLICATION NUMBER: PCT/US99/30095
;; PRIOR FILING DATE: 1999-12-16
;; PRIOR APPLICATION NUMBER: PCT/US99/30911
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US99/30999
;; PRIOR FILING DATE: 1999-12-20
;; PRIOR APPLICATION NUMBER: PCT/US00/00219

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; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 376
; LENGTH: 997
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-902-775A-376

Alignment Scores:
Pred. No.: 7,27e-88      Length: 997
Score: 774.00           Matches: 143
Percent Similarity: 79.07%      Conservative: 27
Best Local Similarity: 66.51%    Mismatches: 43
Query Match: 65.65%            Indels: 2
DB: 2                       Gaps: 2

US-10-812-620-2 (1-214) x US-09-902-775A-376 (1-997)

Qy 1 MetAsnSerThrLysSerProAlaSerHisThrGluArgGlyCysPheLysAsnSer 20
Db 106 ATGATTCATCTAATCATCTGAAACACAATGCACAGAGAGAGATGCTTC---TCTTCC 162

Qy 21 GlnValLeuSerTrpThrIleAlaSerIleLeuPheLeuSerGlyCysPheIle 40
Db 163 CAAATGTTCTTATGGACTGTTGCTGGATCCCATCTATTCTCAGTGCCTGTTTCATC 222

Qy 41 ThrArgCysValValThrTyrArgSerSerGlnIleSerGlyGln---AsnLeuGlnPro 59
Db 223 ACCAGATGTTGTGACATTTTCGCATCTTTCAACCTGTGTAGAGAAAAAGTTTCAGCTA 282

Qy 60 HisArgAsnIleLysGluLeuSerCysTyrSerGluAlaSerGlySerValLysAsnCys 79
Db 283 CCTGAGAATTTTCACAGAGCTCTCTGCTACAAATATGATCAGGTTCAGTCAAGATGTT 342

Qy 80 CysProLeuAsnTrpLysHisTyrGlnSerSerCysTyrPhePheSerThrThrLeu 99
Db 343 TGTCCATGAACTGGGAATATTTTCAATCCAGCTGCTACTTCTTTTCTACTGACACCATT 402

Qy 100 ThrTrpSerSerSerLeuLysAsnCysSerAspMetGlyAlaHisLeuValLilleAsp 119
Db 403 TCTTGGGCGTTAAGTTTAAAGAACTGCTCAGCCATGGGGGCTCACCCTGGTGTATCAAC 462

Qy 120 ThrGlnGluGlnGluPheLeuPheArgThrLysProLysArgLysGluPheTyrIle 139
Db 463 TCACAGAGGAGCAGGAATCTCTTCCTACAGAAACCTAAATAGAGAGTATTTTATT 522

Qy 140 GlyLeuThrAspGlnValValGluGlyGlnTrpGlnTrpValAspAspThrProPheThr 159
Db 523 GGACTGTTCAGACAGAGTTGTCGAGGTCAGTGGCAATGGTGGACGGCACACCTTTGACA 582

Qy 160 GluSerLeuSerPheTrpAspAlaGlyGluProAsnAsnIleValLeuValGluAspCys 179
Db 583 AAGTCTCTGAGTCTTGGGATGTAGGGGAGCCCAACACATAGTACCCCTGGAGGAGCTGT 642

Qy 180 AlaThrIleArgAspSerSerAsnSerArgLysAsnTrpAsnAspIleProCysPheTyr 199
Db 643 GCCACCATGAGAGACTCTTCAAAACCAAGCAAAATGGAAATGATGTAACCTGTTTCCTC 702

Qy 200 SerMetProTrpIleCysGluMetProGluIleSerProLeuAsp 214
Db 703 AATTATTTTCGGATTGTGAAATGGTAGGAATAAATCCTTTGAAC 747

RESULT 4
US-09-906-700-376
; Sequence 376, Application US/09906700
; Patent No. 6723535
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
```

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Alignment Scores:
Pred. No.: 7,27e-88      Length: 997
Score: 774.00           Matches: 143
Percent Similarity: 79.07%      Conservative: 27
Best Local Similarity: 66.51%    Mismatches: 43
Query Match: 65.65%            Indels: 2
DB: 2                       Gaps: 2
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US-10-812-620-2 (1-214) x US-09-906-700-376 (1-997)
Qy 1 MetAsnSerThrLysSerProAlaSerHisThrGluArgGlyCysPheLysAsnSer 20
Db 106 ATGAATTCATCTAAATCATCTGAACACAACTGCAGAGAGAGGATGCTTC--TCTTCC 162
Qy 21 GlnValLeuSerThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle 40
Db 163 CAATATGTTCTTATGGACTGTGCTGGGATCCCATCTCTATTCTCAGTGCCTGTTTTCATC 222
Qy 41 ThrArgCysValValThrTyrArgSerSerGlnIleSerGlyGln--AsnLeuGlnPro 59
Db 223 ACCAGATGTGTGTGACATTTCCGATCTTTCAACCTGTGTGATGAGAAAAGTTTCAGCTA 282
Qy 60 HisArgAsnIleLysGluLeuSerCysTyrSerGluAlaSerGlySerValLysAsnCys 79
Db 283 CCTGAGAATTTTCACAGAGCTCTCCTGCTACAAATTCAGTTCAGTTCAGTCAAGAAATGT 342
Qy 80 CysProLeuAsnThrLysHisTyrGlnSerSerCysTyrPhePheSerThrThrLeu 99
Db 343 TGTCCATTGAACTGGGAATATTTTCAATCCAGCTGCTACTTCTTTCTACTGACACCAATT 402
Qy 100 ThrTrpSerSerLeuLysAsnCysSerAspMetGlyAlaHisLeuValValIleAsp 119
Db 403 TCCTGGGGCTTAAGTTTAAAGAACTGCTACGCCATGGGGGCTCACCTGGTGGTTATCAAC 462
Qy 120 ThrGlnGluGlnGluPheLeuPheArgThrLysProLysArgLysGluPheTyrIle 139
Db 463 TCACAGGAGGACAGGAATTCCTTCTTACAAAGAACTTAAATGAGAGAGCTTTTATT 522
Qy 140 GlyLeuThrAspGlnValValGluGlnTrpGlnTrpValAspAspThrProPheThr 159
Db 523 GGACTGTGACAGACCAAGTTGTGAGGGTCAGTGGCAATGGGTGGACGGCACACCTTTGACA 582
Qy 160 GluSerLeuSerPheTrpAspAlaGlyClnProAsnIleValLeuValGluAsnCys 179
Db 583 AAGTCTCTGAGCTTCTGGGATGTAGGGAGGCCCAACACATATGCTACCTGGAGGACTGT 642
Qy 180 AlaThrIleArgAspSerSerAsnSerArgLysAsnTrpAsnAspIleProCysPheTyr 199
Db 643 GCCACCATGAGAGACTCTTCAACCCCAAGGCAAAATGGGAATGATGTAACCTGTTCTC 702
Qy 200 SerMetProTrpIleCysGluMetProGluIleSerProLeuAsp 214
Db 703 AATTATTTTCGGATTTGTGAATGCTAGGAATAAATCCTTTGAAC 747

RESULT 5
US-09-903-603A-376
; Sequence 376, Application US/09903603A
; Patent No. 6767995
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: GNE.1618P2C12
; CURRENT APPLICATION NUMBER: US/09/903.603A
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; SEQ ID NO 376
; LENGTH: 997
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-903-603A-376
Alignment Scores:
Pred. No.: 7,27e-88 Length: 997
Score: 774.00 Matches: 143
Percent Similarity: 79.07% Conservative: 27
Best Local Similarity: 66.51% Mismatches: 43
Query Match: 65.65% Indels: 2
DB: 4 Gaps: 2
US-10-812-620-2 (1-214) x US-09-903-603A-376 (1-997)
Qy 1 MetAsnSerThrLysSerProAlaSerHisThrGluArgGlyCysPheLysAsnSer 20
Db 106 ATGAATTCATCTAAATCATCTGAACACAACTGCAGAGAGAGGATGCTTC--TCTTCC 162
Qy 21 GlnValLeuSerThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle 40
Db 163 CAATATGTTCTTATGGACTGTGCTGGGATCCCATCTCTATTCTCAGTGCCTGTTTTCATC 222
Qy 41 ThrArgCysValValThrTyrArgSerSerGlnIleSerGlyGln--AsnLeuGlnPro 59
Db 223 ACCAGATGTGTGTGACATTTCCGATCTTTCAACCTGTGTGATGAGAAAAGTTTCAGCTA 282
Qy 60 HisArgAsnIleLysGluLeuSerCysTyrSerGluAlaSerGlySerValLysAsnCys 79
Db 283 CCTGAGAATTTTCACAGAGCTCTCCTGCTACAAATTCAGTTCAGTTCAGTCAAGAAATGT 342
Qy 80 CysProLeuAsnThrLysHisTyrGlnSerSerCysTyrPhePheSerThrThrLeu 99
Db 343 TGTCCATTGAACTGGGAATATTTTCAATCCAGCTGCTACTTCTTTCTACTGACACCAATT 402
Qy 100 ThrTrpSerSerLeuLysAsnCysSerAspMetGlyAlaHisLeuValValIleAsp 119
Db 403 TCCTGGGGCTTAAGTTTAAAGAACTGCTACGCCATGGGGGCTCACCTGGTGGTTATCAAC 462
Qy 120 ThrGlnGluGlnGluPheLeuPheArgThrLysProLysArgLysGluPheTyrIle 139
Db 463 TCACAGGAGGACAGGAATTCCTTCTTACAAAGAACTTAAATGAGAGAGCTTTTATT 522
Qy 140 GlyLeuThrAspGlnValValGluGlnTrpGlnTrpValAspAspThrProPheThr 159
Db 523 GGACTGTGACAGACCAAGTTGTGAGGGTCAGTGGCAATGGGTGGACGGCACACCTTTGACA 582
Qy 160 GluSerLeuSerPheTrpAspAlaGlyClnProAsnIleValLeuValGluAsnCys 179
Db 583 AAGTCTCTGAGCTTCTGGGATGTAGGGAGGCCCAACACATATGCTACCTGGAGGACTGT 642
Qy 180 AlaThrIleArgAspSerSerAsnSerArgLysAsnTrpAsnAspIleProCysPheTyr 199
Db 643 GCCACCATGAGAGACTCTTCAACCCCAAGGCAAAATGGGAATGATGTAACCTGTTCTC 702
Qy 200 SerMetProTrpIleCysGluMetProGluIleSerProLeuAsp 214
Db 703 AATTATTTTCGGATTTGTGAATGCTAGGAATAAATCCTTTGAAC 747
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Db 283 CCTGAGAAATTCACAGAGCTCTCTGCTACAAATATTGGATCAGGTTCAAGAATTGT 342
Qy 80 CysProLeuAsnTrpLysHisIstYrGlnSerSerCysTyrPhePheSerThrThrLeu 99
Db 343 TGTCAATTAAGTGAATATTTTCAATCCAGCTGCTACTTCTTTCTACTGACCACTT 402
Qy 100 ThrTrpSerSerSerLeuLysAsnCysSerAspMetGlyAlaHisLeuValValIleAsp 119
Db 403 TCTCGGCGTTAAGTTTAAAGACTGCTCAGCCATGGGGGCTCACTGGTGGTTATCAAC 462
Qy 120 ThrGlnGluGlnGlnPheLeuPheArgThrLysProLysArgLysGluPheTyrIle 139
Db 463 TCACAGGAGGAGCAGAAATCTCTTCCCTACAAGAAACCTAAATGAGAGAGTTTTTATT 522
Qy 140 GlyLeuThrAspGlnValValGluGlnGlnTrpGlnTrpValAspThrProPheThr 159
Db 523 GCACTGTCTACAGCAGGTTGTCAGGGTTCAGTGGCAATGGTGGCAGCCACCTTTTGACA 582
Qy 160 GluSerLeuSerPheTrpAspAlaGlyGluProAsnAsnIleValLeuValGluAspCys 179
Db 583 AGTCTCTGAGTCTTGGGATGTAGGGGAGCCCAACATAGCTACCTGGAGGACTGT 642
Qy 180 AlaThrIleArgAspSerSerAsnSerArgLysAsnTrpAsnAspIleProCysPheTyr 199
Db 643 GCCACCATGAGAGACTCTTCAAAACCCAGGCAAAATTTGGAATGATGTAACCTGTTTCTCTC 702
Qy 200 SerMetProTrpIleCysGluMetProGluIleSerProLeuAsp 214
Db 703 AATTATTTTCGAGTTTGTGAATGTTAGAGAAATAAATCTCTTGAAC 747

RESULT 6

US-09-904-920A-376

; Sequence 376, Application US/09904920A

; Patent No. 6806352

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, A.

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth, J.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Mather, Jennie P.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William, I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: 10466-14

; CURRENT APPLICATION NUMBER: US/09/904,920A

; CURRENT FILING DATE: 2001-07-13

; PRIOR APPLICATION NUMBER: PCT/US00/04414

; PRIOR FILING DATE: 2000-02-22

; PRIOR APPLICATION NUMBER: US 60/143,048

; PRIOR FILING DATE: 1999-07-07

; PRIOR APPLICATION NUMBER: US 60/145,698

; PRIOR FILING DATE: 1999-07-26

; PRIOR APPLICATION NUMBER: US 60/146,222

; PRIOR FILING DATE: 1999-07-28

; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 376
; LENGTH: 997
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-904-920A-376

Alignment Scores:
Pred. No.: 7,27e-88 Length: 997
Score: 774.00 Matches: 143
Percent Similarity: 79.07% Conservative: 27
Best Local Similarity: 66.51% Mismatches: 43
Query Match: 65.65% Indels: 2
DB: 4 Gaps: 2

US-10-812-620-2 (1-214) x US-09-904-920A-376 (1-997)

Qy 1 MetAsnSerThrLysSerProAlaSerHisHisThrGluArgGlyCysPheLysAsnSer 20
Db 106 ATGAATTCATCTAATCATCTGAAACAAATGCACAGAGAGAGATGCTTC---TCTTCC 162
Qy 21 GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle 40
Db 163 CAAATGTTCTTATGGACTGTTGCTGGGATCCCATCTTATTTCTCAGTGCCTGTTTCATC 222
Qy 41 ThrArgCysValValThrThrArgSerSerGlnIleSerGlyGln---AsnLeuGlnPro 59
Db 223 ACCAGATGTTGTTGACATTTTCGATCTTTCAAAACCTGTGATGAGAAAAAGTTTCAGCTA 282
Qy 60 HisArgAsnIleLysGluLeuSerCysTyrSerGluAlaSerGlySerValLysAsnCys 79
Db 283 CCTGAGAAATTTCAACAGAGCTCTCTCTGCTACAAATATGATTCAGTTCAAGATTTGT 342
Qy 80 CysProLeuAsnTrpLysHisIstYrGlnSerSerCysTyrPhePheSerThrThrLeu 99
Db 343 TGTCAATTAAGTGAATATTTTCAATCCAGCTGCTACTTCTTTCTACTGACCACTT 402
Qy 100 ThrTrpSerSerSerLeuLysAsnCysSerAspMetGlyAlaHisLeuValValIleAsp 119
Db 403 TCTCGGCGTTAAGTTTAAAGACTGCTCAGCCATGGGGGCTCACTGGTGGTTATCAAC 462
Qy 120 ThrGlnGluGlnGlnPheLeuPheArgThrLysProLysArgLysGluPheTyrIle 139
Db 463 TCACAGGAGGAGCAGAAATCTCTTCCCTACAAGAAACCTAAATGAGAGAGTTTTTATT 522
Qy 140 GlyLeuThrAspGlnValValGluGlnGlnTrpGlnTrpValAspThrProPheThr 159

APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mathet, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/306,618
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2001-07-16
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
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PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
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PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 376
LENGTH: 997
TYPE: DNA
ORGANISM: Homo Sapien
US-09-906-618-376

Alignment Scores:
Pred. No.: 7,27e-88 Length: 997
Score: 774.00 Matches: 143
Percent Similarity: 79.07% Conservative: 27
Best Local Similarity: 66.51% Mismatches: 43
Query Match: 65.65% Indels: 2
DB: 4 Gaps: 2

US-10-812-620-2 (1-214) x US-09-906-618-376 (1-997)

Qy 1 MetAenSerThrLysSerProAlaSerHisThrGluArgGlyCysPheLysAenSer 20
Db 106 ATGAATTCATCTAAATCTGTAACACCAATGACAGAGAGAGATGCTTC---TCTTCC 162
Qy 21 GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle 40

Db 163 CAAATGTTCTTATGGACTGTGTGGGATCCCATCTCTATTTCTCAGTGCCTGTTTCATC 222
Qy 41 ThrArgCysValValThrTyArgSerSerGlnIleSerGlyGln---AenLeuGlnPro 59
Db 223 ACCAGATGTTGTGACATTCGGATCTTTCAACCTGTGATGAGAAAAGTTTCAGGTA 282
Qy 60 HisArgAenIleLysGluLeuSerCysTySerGluAlaSerGlySerValLysAenCys 79
Db 283 CCTGAGAATTTTCACAGAGCTCTCTCTGCTACAATTTATGGATTCAGGTTTCAGTCAAGAATGT 342
Qy 80 CysProLeuAenTrpLysHisTyArgSerSerCysTySerPhePheSerThrThrLeu 99
Db 343 TGTCATTTGAACCTGGGAATATTTTCAATCCAGCTGCTACTTCTTTCTACTGACACCAT 402
Qy 100 ThrTrpSerSerLeuLysAenCysSerAspMetGlyAlaHisLeuValValIleAep 119
Db 403 TCCTGGCGTTAAGTTTAAAGAACTGCTCAGCCATGGGGCTCAGCTGGTGGTTATCAAC 462
Qy 120 ThrGlnGluGlnGluPheLeuPheArgThrLysProLysArgLysGluPheTyrlle 139
Db 463 TCACAGGAGGAGCAGGAATTCCTTCTCACAAGAAACCTAAATGAGAGAGATTTTATT 522
Qy 140 GlyLeuThrAspGlnValValGluGlyGlnTrpGlnTrpValAspAspThrProPheThr 159
Db 523 GGACTGTCAGACCCAGGTTGTCAGGGTCAGTGGCAATGGGTGGACGGCACACCTTTGACA 582
Qy 160 GluSerLeuSerPheTrpAspAlaGlyGluProAenAenIleValLeuValGluAspCys 179
Db 583 AAGTCTCTGAGCTTCTGGGATGTAGGGGAGCCCAACACATAGCTACCTGGAGGAGCTGT 642
Qy 180 AlaThrIleArgAspSerSerAsenSerArgLysAenTrpAenAspIleProCysPheTyrl 199
Db 643 GCCACCATGAGAGACTCTTCAACCCCAAGGCAAAATTTGGAATGATGTAACCTGTTTCCTC 702
Qy 200 SerMetProTrpLysCysGluMetProGluLysSerProLeuAep 214
Db 703 AATTATTTTCGGATTTGTGAATGGTAGGAATAAATCCTTTGAAC 747

RESULT 10
US-08-772-440-3
Sequence 3, Application US/08772440
Patent No. 6046158
GENERAL INFORMATION:
APPLICANT: Arizumi, Kiyoshi
APPLICANT: Takashima, Akira
TITLE OF INVENTION: UNIQUE DENDRITIC CELL-ASSOCIATED C-TYPE
TITLE OF INVENTION: LECTINS, DEXTIN-1 AND DEXTIN-2; COMPOSITIONS AND USES
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/772,440
FILING DATE: CONCURRENTLY HERewith
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: UTXD:493
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577


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; TITLE OF INVENTION: LECTINS, DECTIN-1 AND DECTIN-2; COMPOSITIONS AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/772,440
; FILING DATE: CONCURRENTLY HERewith
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, David L.
; REGISTRATION NUMBER: 32,165
; REFERENCE/DOCKET NUMBER: UTXXD:493
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 501 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-772-440-20

Alignment Scores:
Pred. No.: 6.66e-33 Length: 501
Score: 336.00 Matches: 67
Percent Similarity: 58.90% Conservative: 29
Best Local Similarity: 41.10% Mismatches: 55
Query Match: 28.50% Indels: 12
DB: 3 Gaps: 3

US-10-812-620-2 (1-214) x US-08-772-440-20 (1-501)

Qy 58 GlnProHisArgAsnIleLysGlu-----LeuSerCysTyrSer 70
Db 13 CAGCCAGTAGACACTATATGAACCTCACATACCATCCAGTCTCAGCTGCTTCACT 72
Qy 71 Glu-----AlaSerGlySerValLysAsnCysCysProLeuAsnTrpLysHisTyr 87
Db 73 GAAGGGACTATGGTGTGCAGAAAAAATGTGGGATGCTGCCAAATCACTGGAAGTCATT 132
Qy 88 GlnSerSerCysTyrPhePheSerThrThrThrLeuThrTrpSerSerSerLeuLysAsn 107
Db 133 GGCTCCAGCTGCTACCTCATTCTTACCAGGAGAACTTCTGGAGCACGAGTGCAGAAC 192
Qy 108 CysSerAspMetGlyAlaHisLeuValValIleAspThrGlnGluGluGlnPheLeu 127
Db 193 TGTGTTTCAGATGGGGGCTCATCTGTGTGATCATCTGAAGCGGAGCAGAAATTCATC 252
Qy 128 PheArgThrLysProLysArgLysGluPheTyrIleGlyLeuThrAspGlnValIleGlu 147
Db 253 ACCCAGCAGCTGAATGACTCTTCTTACTTCCTGGGTCTTTCGGATCCACAGGTAAT 312
Qy 148 GlyGlnTrpGlnTrpValAspAspThrProPheThrGluSerLeuSerPheTrpAspAla 167
Db 313 GGCAATGGCAATGGATCGATGATCTCTTCACTCAAAATGTGAGTCTGTCGACCCC 372
Qy 168 GlyGluProAsnAsnIleValLeuValGluAspCysAlaThrIleArgAspSerSerAsn 187
Db 373 CATGAACCCAAAT-----CITCCAGAGAGAGGGGTGTTTCAATAGTATTACTGGAATCCT 426
Qy 188 SerArgLysAsnTrpAsnAspIleProCysPheTyrSerMetProTrpIleCysGluMet 207
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Db 427 TCGAATGGCGCTGGAATGATGTTTCTGTGATAGTAACACAAATTCATATGTGAATG 486
Qy 208 ProGluile 210
Db 487 AAGAGATT 495

RESULT 13
US-09-111-470-1
; Sequence 1, Application US/09111470
; Patent No. 6277959
; GENERAL INFORMATION:
; APPLICANT: Valladeau, Jenny
; APPLICANT: Ravel, Odile
; APPLICANT: Bates, Elizabeth E.M.
; APPLICANT: Ford, John
; APPLICANT: Saeland, Sem
; APPLICANT: Lebecque, Serge J.E.
; TITLE OF INVENTION: Mammalian Membrane Protein Genes;
; TITLE OF INVENTION: Related Reagents
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/111,470
; FILING DATE: 08-JUL-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/053,080
; FILING DATE: 09-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: SF0695
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650)852-9196
; TELEFAX: (650)496-1200
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1104 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 242..952
; US-09-111-470-1

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Score: 325.50 Matches: 72
Percent Similarity: 49.31% Conservative: 35
Best Local Similarity: 33.18% Mismatches: 101
Query Match: 27.61% Indels: 9
DB: 3 Gaps: 4

US-10-812-620-2 (1-214) x US-09-111-470-1 (1-1104)

Qy 1 MetAsnSerThrLysSerProAlaSerHisThrGluArgGlyCysPheLysAsnSer 20
Db 302 ATCAACACAGCCCTTCTCGAGCTTCCAGGAGGAGGACTGCCCTCTCAAAAGTAATACC 361
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Qy	21	GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeu-----SerGly	37
Db	362	GGATTCCCCAAGCTGCTTTGTGCCTCACTGTTGATATATTTTCTCGTATTGGCAATCTCA	421
Qy	38	CysPheIleThrArgCysValValThrTyArgSerSerGlnIleSerGlyGlnAsnLeu	57
Db	422	TTCTTTATTGCTTTGTCTCAITTTCTTCAAAATATATCTCGACTCTTTGAAAAAAGACT	481
Qy	58	GlnProHisArgAsnIleLysGluLeuSerCysTySerSerGlu-----AlaSerGly	74
Db	482	ACAAAGAGCTGGTTCATACACATTTGGAGTGTGTGAAAAAATAATGCCCGTGGAGAG	541
Qy	75	SerValLysAsnCysCysProLeuAsnTrpLysHisTyGlnSerSerCysTySerPhePhe	94
Db	542	ACAGCCTGGAGCTGTTGCCCAAGAAATTTGGAAGTCATTTAGTTCCAACTGCTACTTTATT	601
Qy	95	SerThrThrThrLeuThrTrpSerSerSerLeuLysAsnCysSerAspMetGlyAlaHis	114
Db	602	TTTACTGAATCAGCATCTTTGGCAAGACAGTGTGAAGGACTGTGTAGAAATGGAGGGCTCAC	661
Qy	115	LeuValValIleAspThrGlnGluGlnGlnGluPheLeuPheArgTrpLysProLysArg	134
Db	662	CTGCTGGTGATAACACTCAAGAAGACGAGGATTTTCATCTTCCAGAACTCTGCAAGAAGAA	721
Qy	135	LysGluPheTyrlleGlyLeuThrAspGlnValValGluGlyGlnTrpGlnTrpValAsp	154
Db	722	TCTGCTATTATTTTGGGGCTCTCAGATCCAGAAGGTCACGCACATGGCAATGGGTTGAT	781
Qy	155	AspThrProPheThrClnSerLeuSerPheTrpAspAlaGlyGluProAsnAsnIleVal	174
Db	782	CAGACACCATACAAATGAAGTTCACATCTCGGCATCCACGCTGAGCCAGTGAT-----	835
Qy	175	LeuValGluAspCysAlaThrIleArg---AspSerSerAsnSerArgLysAsnTrpAsn	193
Db	836	CCCAATGAGCGTGGCTGTGCTAAATTTTCGTAAATCACCCAAAAGATGGGGCTGGAT	895
Qy	194	AspIleProCysPheTySerMetProTrpIleCysGluMetProGluIle	210
Db	896	GATGTTAAATTTGCTTGGTCTCTCAAAAGGTCAAGTTTGTGAGATGATGAAGATC	946

RESULT 14

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US-09-862-802A-1
; Sequence 1, Application US/09862802A
; Patent No. 6756478
; GENERAL INFORMATION:
; APPLICANT: Valladeau, Jenny
; APPLICANT: Ravel, Odile
; APPLICANT: Bates, Elizabeth Ester Mary
; APPLICANT: Ford, John
; APPLICANT: Lebecque, Serge J.E.
; APPLICANT: Saeland, Sem
; TITLE OF INVENTION: Isolated Mammalian Membrane Protein Genes; Related Reagents
; FILE REFERENCE: SF0695 B
; CURRENT APPLICATION NUMBER: US/09/862,802A
; CURRENT FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/053,080
; PRIOR FILING DATE: 1997-07-09
; PRIOR APPLICATION NUMBER: US 09/111,470
; PRIOR FILING DATE: 1998-07-08
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1104
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: mammalian nucleic acid and protein
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (242)..(952)
; OTHER INFORMATION:
; US-09-862-802A-1

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Alignment Scores:
Pred. No.: 5,09e-31 Length: 1104
Score: 325.50 Matches: 72
Percent Similarity: 49.31% Conservative: 35
Best Local Similarity: 33.18% Mismatches: 101
Query Match: 27.61% Indels: 9
DB: 4 Gaps: 4

US-10-812-620-2 (1-214) x US-09-862-802A-1 (1-1104)

QY 1 MetAenSerThrLysSerProAlaSerHisThrGluArgGlyCysPheLysAenSer 20
AT:::|||||
Db 302 ATCAACACAGCGCTCTTCGCAGCTTCCAAAGGAGAGACTGCCCTCTCAAAGTAGTAATCC 361
|||
QY 21 GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeu-----SerGly 37
GGATTCCCCAGCTGCTTTGGCCTCACGTGTGTATATTTTCTGCTATTGGCAATCTCA 421
|||
Db 362 GGATTCCCCAGCTGCTTTGGCCTCACGTGTGTATATTTTCTGCTATTGGCAATCTCA 421
|||
QY 38 CysPheIleThrArgCysValValThrTyrrArgSerSerGlnIleSerGlyGlnAenLeu 57
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Db 422 TTCCTTATTGCTTTTGTCATTTCTTCCAAAATAATCTCAGCTTCTTGAAAAAAGACT 481
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QY 58 GlnProHisArgAenIleLysGluLeuSerCysTyrrSerGlu-----AlaSerGly 74
ATCAAAAGAGCTGGTTCATACAACTGGAGTGTGTGAAAAAAATATGCCCTGGGAAGAG 541
|||
Db 482 ACAAAGAGCTGGTTCATACAACTGGAGTGTGTGAAAAAAATATGCCCTGGGAAGAG 541
|||
QY 75 SerValLysAenCysPheProLeuAenTrpLysHisTyrrGlnSerSerCysTyrrPhePhe 94
:::|||||
Db 542 ACAGCTGGAGCTGTTGCCCAAGNATTTGGAAAGTCATTAGTTCCAACCTGCTACTTTATT 601
|||
QY 95 SerThrThrLeuLeuThrTrpSerSerSerLeuLysAenCysSerAspMetGlyAlaHis 114
|||||:::
Db 602 TCTACTGAATCAGCATCTTGCAACAGCAGTGAGAAGGACTGTGTAGAAATGGAGGCTCAC 661
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QY 115 LeuValValIleAspThrGlnGluGlnGluPheLeuPheArgThrLysProLysArg 134
|||||:::
Db 662 CTGCTGGTGATAAACACTCAAGAGAGCAGGATTTTCATCTCCAGAAATCTGCAAGAA 721
|||
QY 135 LysGluPheTyrrIleGlyLeuThrAspGlnValValGluGlyGlnTrpGlnTrpValAsp 154
:::|||||
Db 722 TCTGCTTATTTTGGGGGCTCTCAGATCCAGNAGTCCAGCNATGGCNATGGGTGTAT 781
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QY 155 AspThrProPheThrGluSerLeuSerPheTrpAspAlaGlyGluProAenAenIleVal 174
|||||:::
Db 782 CAGACACCATACAATGAAGATCCACATCTTGGCATCCAGCTGAGGCCAGCTGAT---- 835
|||
QY 175 LeuValGluAspCysAlaThrIleArg---AspSerSerAenSerArgLysAenTrpAen 193
|||||:::
Db 836 CCCAATGACGCTGGTGTGTGCTAAATTTTCGTAAATCACCACCAAGATGGGGCTGGAAT 895
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QY 194 AspileProCysPheTyrrSerMetProTrpIleCysGluMetProGluIle 210
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Db 896 GATGTTAATTGCTTGGTCTCAAAGGTCAGTTTGTGAGATGATGAAGATC 946
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RESULT 15
US-09-489-847-119
; Sequence 119 Application US/09489847
; Patent No. 6476195
; GENERAL INFORMATION:
; APPLICANT: Rosen et al
; TITLE OF INVENTION: 98 Human Secreted Proteins
; FILE REFERENCE: PZ031Pl
; CURRENT APPLICATION NUMBER: US/09/489,847
; CURRENT FILING DATE: 2000-01-24
; EARLIER APPLICATION NUMBER: PCT/US99/17130
; EARLIER FILING DATE: 1999-07-29
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; EARLIER APPLICATION NUMBER: 60/095,486
; EARLIER FILING DATE: 1998-08-05
; EARLIER APPLICATION NUMBER: 60/096,319
; EARLIER FILING DATE: 1998-08-12
; EARLIER APPLICATION NUMBER: 60/095,454

; EARLIER FILING DATE: 1998-08-06
; EARLIER APPLICATION NUMBER: 60/095,455
; EARLIER FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 376
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 119
; LENGTH: 2059
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-489-847-119

Alignment Scores:
Pred. No.: 5,33e-29 Length: 2059
Score: 313.00 Matches: 80
Percent Similarity: 56.93% Conservative: 35
Best Local Similarity: 39.60% Mismatches: 72
Query Match: 26.55% Indels: 16
DB: 4 Gaps: 4

US-10-812-620-2 (1-214) x US-09-489-847-119 (1-2059)

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Db 105 CAGCTGATACCTTCGGTTATTGCTGTAGTTTTCATCTTACTTCTCGGTGCTGTTTATT 164
Qy 41 ThrArgCysValThrTyr-----ArgSerSerGlnIleSerGly---Gln 55
Db 165 GCAAGTTGTTGGTGACTCATCAAACTTTTCACGCTGTAAGAGAGGCACAGGAGTGCAC 224
Qy 56 AsnLeuGlnProHis-----ArgAsnIleLysGluLeuSerCysTyrSerGlu-Al 72
Db 225 AAGTTAGAGCACCATCAAAAGCTCAAAATGTCATCAAGAGAAATCAGAACTGAAAAGTTGC 284
Qy 72 aSerGlySerValLysAsnCysProLeuAsnTrpLysHisTyrGln-SerSerCyst 92
Db 285 TGAAGGGAGCACCTGGAACTGTGTCTATTGACTGGAGAACCTTCCAGTTCCAACTGCT 344
Qy 92 Yr-PhePheSerThrThrLeuThrTrpSerSerLeuLys-AsnCysSerAspMe 111
Db 345 ATTTTCTCTCTTACTGACAAACAGACGTGGGCTGAGAGTTGAAAGGAACCTGTTCAGGGAT 404
Qy 111 tGlyAlaHisLeuValValIleAspThrGlnGluGlnGluPheLeuPheArgThrLy 131
Db 405 GGGGGCCCATCTGATGACCATCAGCACGGAAGCTGAGCAGAACTTTATTATTCACTTCT 464
Qy 131 sProLysArgLysGluPheTyrIleGlyLeuThrAspGlnValValGluGlyGlnTrpGl 151
Db 465 GGATAGACGGCTTCTCTATTTCCTTGGACTTGGAGATGAGAAATGCCAAAGGTCAAGTGGCG 524
Qy 151 nTrpVal-AspAspThrProPhe-ThrGluSerLeuSerPheTrpAspAlaGlyGluPro 170
Db 525 TTGGGTGGGACACAGCCCATTTAAACCCACGCCAGAGTATTCTGGCATAGAATGAACCC 584
Qy 171 AsnAsnIleValLeuValGluAspCysAlaThrIleArgAspSerSerAsnSerArgLys 190
Db 585 GACAAC---TTCAGGGAGAAAACCTGTGTTCTCTGG--TCTTATAACCAAGATAAAATGG 639
Qy 191 AsnTrpAsnAspIleProCysPheTyr-SerMetProTrpIleCysGluMetPro 208
Db 640 GCCTGGGAATGATGTCTCTTGAACCAAGTAGGATTTGTAATAATACCT 693
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Job time : 194 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 9, 2005, 09:46:10 ; Search time 4143 Seconds
(without alignments)
2502.876 Million cell updates/sec

Title: US-10-812-620-2

Perfect score: 1179

Sequence: 1 MNSTKSPASHHTGCGFKNS.....IPCFYMPWICEMPEISPLD 214

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Ygapop 10.0			0.5
Ygapop 6.0			7.0
Deiop 6.0			7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=BLOSUM62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -NAXLEN=200000000
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Database :

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2: gb_btg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sta.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1179	100.0	2517	10_ AB024717	Mus muscu
3	1149	97.5	2517	6_ E54035	Novel C lec
4	1149	97.5	2517	6_ BD094039	A novel C

ALIGNMENTS

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DEFINITION	BC003218	Mus musculus C-type (calcium dependent, carbohydrate recognition domain) lectin, superfamily member 9, mRNA (cdna clone MGC:5682 IMAGE:3158063), complete cds.		
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VERSION	BC003218.1	GI:13096843		
KEYWORDS	MGC.			
SOURCE	Mus musculus (house mouse)			
ORGANISM	Mus musculus			
REFERENCE	1 (bases 1 to 1606)			
AUTHORS	Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Scapleton, M., Soares, N.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,			

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smallos, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

TITLE
JOURNAL
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL

12477932
2 (bases 1 to 1606)
Straussberg, R.

Direct Submission

Submitted (20-FEB-2001) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Jeffrey Green M.D.

CDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing Arrayed by: The I.M.A.G.E. Consortium (LLNL)

Sequencing Center

Center code: BCM-HGSC

Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>

Contact: ang@bcm.tmc.edu

Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Louleoged, H.,

Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,

A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found

through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAC Plate: 6 Row: 1 Column: 23

This clone was selected for full length sequencing because it

passed the following selection criteria: matched mRNA gi: 9910161.

Location/Qualifiers

1. .1606

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/mol_type="mRNA"

/strain="FVB/N"

/db_xref="taxon:10090"

/clone="MGC:5682 IMAGE:3158063"

/tissue_type="Mammary tumor. C3(1) -Tag model. Infiltrating

ductal carcinoma. 5 month old virgin mouse."

/clone_lib="NCI_CGAP_Mam6"

/lab_host="DH10B"

/note="Vector: pCMV-SPORT6"

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/gene="Clec4e9"

/note="synonym: Mincle"

/db_xref="LocusID:56619"

/db_xref="MGI:1861232"

82. .726

/gene="Clec4e9"

/codon_start=1

/product="C-type lectin, superfamily member 9"

/protein_id="AAH03218.1"

/db_xref="GI:13096844"

/db_xref="LocusID:56619"

/db_xref="MGI:1861232"

/translation="WNSTKSPASHHTGCKFNKSOVLWTLGASILFLSGCFITRCV

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SLSFWDGEPNNVLVEDCATIRDSNRKNWDIPCFYSNPWICEMPEISPLD"

ORIGIN

Alignment Scores:

Pred. No.: 3,38e-111 Length: 1606
Score: 1179.00 Matches: 214
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 10 Gaps: 0

US-10-812-620-2 (1-214) x BC003218 (1-1606)

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QY 21 GlnValLeuSerTptThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCyshelle 40
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QY 41 ThrArgCysValValThrTyrArgSerSerGlnIleSerGlyGlnAsnLeuGlnProHis 60
DB 202 ACCAGATGTGTCTAACAATATCGAGCTCTCAATTCGGGCGAGAACTTACAGCCAT 261
QY 61 ArgAenIleLysGluLeuSerCysTyrSerGluAlaSerGlySerVallyAenCys 80
DB 262 AGAATAATTAAGGAGCTTTCTCTGTACAGTGAGGCATCAGGTTCAAGAAATGCTGT 321
QY 81 ProLeuAenTptLysHisTyrGlnSerSerCysTyrPhePheSerThrThrLeuThr 100
DB 322 CTTTGAACCTGGAAACATTAATCTAGTTGTATTTTCTCTTACGACCACTTGACC 381
QY 101 TptSerSerSerLeuLysAenCysSerAspMetGlyAlaHisLeuValValIleAspThr 120
DB 382 TGGTCATCAAGTTTAAAGAAATGCTCAGACATGGGGCTCACCTGTGTATTCACACA 441
QY 121 GlnGluGlnGlnGluPheLeuPheArgThrLysProLysArgLysGluPheTyrIleGly 140
DB 442 CAGGAAGAGCAGGAATCTCTTTTCGACAAAAACCTAAAGAGAAAGAGTTTATATGGA 501
QY 141 LeuThrAapGlnValValGlyGlnTrpGlnTrpValAapAapThrProPheThrGlu 160
DB 502 CTGACAGACACAGGTGGTGGAGGTCAGTGGCAATGGGTGGATGATACACCTTTTACAGAG 561
QY 161 SerLeuSerPheTptAspAlaGlyGluProAenAenIleValLeuValGluAapCysAla 180
DB 562 TCCCTGAGCTCTGGGATGCTGGGAGGCCCAACAATATAGTTTGTGGAGGAGCTGTGCC 621
QY 181 ThrIleArgAapSerSerAsnSerArgLysAenTrpAenAapIleProCysPheTyrSer 200
DB 622 ACCATAAGGAGCTCTTCAAACTCCAGGAAGAACTGGAAATGATATATACCTGTTTCTACAGT 681
QY 201 MetProTptLysCysGluMetProGluIleSerProLeuAap 214
DB 682 ATGCTTGGATTGTGAGATGCCAGAAATAAGTCTCTCTGGAC 723

RESULT 2

AB024717

LOCUS

DEFINITION

cds.

AB024717

VERSION

AB024717.1

KEYWORDS

Mincle; macrophage C-type lectin Mincle.

SOURCE

Mus musculus (house mouse)

ORGANISM

Mus musculus

REFERENCE

1 (sites)

AUTHORS

Gilbert, D.J., Jenkins, N.A. and Akira, S.

A novel LPS-inducible C-type lectin is a transcriptional target of

NF-IL6 in macrophages

J. Immunol. 163 (9), 5039-5048 (1999)

JOURNAL

MEDLINE

99458965

PUBMED

10528209

REFERENCE

2 (bases 1 to 2517)

Akira, S. and Matsumoto, M.

Direct Submission

TITLE

Submitted (09-MAR-1999) Shizuoka Akira, Osaka University, Department

JOURNAL

of Host Defense, Research Institute for Microbial Diseases; 3-1

Yamada-oka, Suita, Osaka 565-0871, Japan

(E-mail: eakira@biken.osaka-u.ac.jp, Tel: 81-6-6879-8303,
Fax: 81-6-6879-8305)

FEATURES

source
Location/Qualifiers
1. .2517
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1. .2517
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124. .768
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ORIGIN

Alignment Scores:
Pred. No.: 5,74e-111 Length: 2517
Score: 1179.00 Matches: 214
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-812-620-2 (1-214) x AB024717 (1-2517)

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Db 184 CAAGTGTCTCTCGAGAGATAGCCGGGGCTCCATCTGTTTCTCAGTGGCTGTTTCAATC 243
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Db 244 ACCAGATGTCTGTAACATATCGAGCTCTCAAAATTTCCGGGACAACTTACAGCCACAT 303
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Qy 81 ProLeuAsnTrpLysHisTyrGlnSerSerCysTyrPhePheSerThrThrLeuThr 100
Db 364 CCTTTGAACCTGGAACATTAATCAATCTAGTTGTTATTTTCTTACGACAACTTGACC 423
Qy 101 TrpSerSerLeuLysAsnCysSerAspMetGlyAlaHisLeuValValIleAspThr 120
Db 424 TGGTCATCAAGTTTAAAGAGCTTCTGCTACAGTGGGCTCACCCTGGTGGTATCGACACA 483
Qy 121 GlnGluGlnGluPheLeuPheArgThrLysProLysArgLysGluPheTyrIleGly 140
Db 484 CAGGAAGAGCAGGAATTTCTTTTCGACAAAACCTTAAAGGAAGATTTATATTTGA 543
Qy 141 LeuThrAspGlnValValGluGlyGlnTrpGlnTrpValAspAspThrProPheThrGlu 160
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Db 564 ACCATAGGAGGACTCTTCAAACTCCAGGAGAACTGGGAATGATATACCTGTTTCTACAGT 723
Qy 201 MetProTrpLysCysGluMetProGluIleSerProLeuAsp 214
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Db 724 ATGCCCTTGGATTCTGAGATGCCAGAAATAAGTCTCTGGAC 765

RESULT 3

E54035
LOCUS
DEFINITION Novel C lectin and gene thereof.
ACCESSION E54035
VERSION E54035.1 GI:22553489
KEYWORDS JP 2001112482-A/1.
SOURCE Mus sp.
ORGANISM Mus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2517)
Shinra, S. and Matsumoto, M.
Novel C lectin and gene thereof
Patent: JP 2001112482-A 1 24-APR-2001;
JOURNAL SCIENCE & TECH AGENCY
COMMENT OS Mus sp. (mouse)
PN JP 2001112482-A/1
PD 24-APR-2001
PF 15-OCT-1999 JP 1999293724
PI SHIZUO SHINRA, MAKOTO MATSUMOTO
PC C12N15/09; A61K38/00; A61P31/00; A61P37/04; A61P43/00; C07K14/47,
PC C12Q1/68,
PC C12N15/00; A61K37/02
CC
FH Key Location/Qualifiers.

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source
1. .2517
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ORIGIN

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Pred. No.: 6,95e-108 Length: 2517
Score: 1149.00 Matches: 209
Percent Similarity: 98.13% Conservative: 1
Best Local Similarity: 97.66% Mismatches: 4
Query Match: 97.46% Indels: 0
DB: 6 Gaps: 0

US-10-812-620-2 (1-214) x E54035 (1-2517)

Qy 1 MetAsnSerThrLysSerProAlaSerHisHisThrGluArgGlyCysPheLysAsnSer 20
Db 124 ATGAATTCACCAAAATCGCTGCATCCACACACAGAGAGGATGCTTCAAAAACCTCC 183
Qy 21 GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle 40
Db 184 CAAGTGTCTCTCGAGAGATAGCCGGGGCTCCATCTGTTTCTCAGTGGCTGTTTCAATC 243
Qy 41 ThrArgCysValValThrTyrArgSerSerGlnIleSerGlyGlnAsnLeuGlnProHis 60
Db 244 ACCAGATGTCTGTAACATATCGAGCTCTCAAAATTTCCGGGACAACTTACAGCCACAT 303
Qy 61 ArgAsnIleLysGluLeuSerCysTyrSerGluAlaSerGlySerValLysAsnCysCys 80
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Qy 81 ProLeuAsnTrpLysHisTyrGlnSerSerCysTyrPhePheSerThrThrLeuThr 100
Db 364 CCTTTGAACCTGGAACATTAATCAATCTAGTTGTTATTTTCTTACGACAACTTGACC 423
Qy 101 TrpSerSerLeuLysAsnCysSerAspMetGlyAlaHisLeuValValIleAspThr 120
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Db 604 TCCCTGACCTCTGGGATGCTGGGAGGCCCAACAATATAGTTTGGTGGAGGACTGTGCC 663
QY 181 ThrIleArgAspSerSerAsnSerArgLysAsnTrpAsnAspIleProCysPheTrpSer 200
Db 664 ACCATAAGGAGCTCTTCAAACTCCAGGAAGAACTGGAATGATAATCCCTGTTTCTACAGT 723
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Db 724 ATGCCCTTGGATTGTGAGATGCCAGNAATAAGTCTCTCAGGAC 765

RESULT 4
BD094039
LOCUS BD094039 2517 bp DNA linear PAT 27-AUG-2002
DEFINITION A novel C-type lectin and its genes.
ACCESSION BD094039
VERSION BD094039.1 GI:22639627
KEYWORDS WO 0127271-A/1.
SOURCE Mus sp.
ORGANISM Mus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1. (bases 1 to 2517)
Akira, S. and Matsumoto, M.
A novel C-type lectin and its genes
Patent: WO 0127271-A 1 19-APR-2001;
JAPAN SCIENCE AND TECHNOLOGY CORP. SHIZUO AKIRA, MAKOTO MATSUMOTO
OS Mus sp. (mouse)
PN WO 0127271-A/1
PD 19-APR-2001
PF 02-OCT-2000 WO 2000JP006820
PR 15-OCT-1999 JP 99P 293724
PI SHIZUO AKIRA, MAKOTO MATSUMOTO
PC C12N15/12,C07K14/47,C12Q1/68,A61K38/17,A61P31/00,A61P37/04, PC
A61P43/00
CC
FH Key Location/Qualifiers.
FEATURES
Source 1..2517
Location/Qualifiers
/organism="Mus sp."
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ORIGIN
Alignment Scores:
Pred. No.: 6,95e-108 Length: 2517
Score: 1149.00 Matches: 209
Percent Similarity: 98.13% Conservative: 1
Best Local Similarity: 97.66% Mismatches: 4
Query Match: 97.46% Indels: 0
DB: 6 Gaps: 0

US-10-812-620-2 (1-214) x BD094039 (1-2517)

QY 1 MetAsnSerThrLysSerProAlaSerHisThrGluArgGlyCysPheLysAsnSer 20
Db 124 ATGAATTCACCAATCGCTGCATCCACACACAGAGAGGATGCTTCAAAAACCTCC 183
QY 21 GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle 40
Db 184 CAAAGTGCTCTCTGGACGATAGCCGGGCTCCATCTGTTTCTCAGTGGCTGTTCATC 243
QY 41 ThrArgCysValValThrTyArgSerSerGlnIleSerGlyGlnAsnLeuGlnProHis 60
Db 244 ACCAGATGTGCTGAACATATCGAGCTCTCAAAATTCGGGCAAGAACTTACAGCCACAT 303
QY 61 ArgAsnIleLysGluLeuSerCysTySerGluAlaSerGlySerValLysAsnCys 80
Db 91 ArgAsnIleLysGluLeuSerCysTySerGluAlaSerGlySerValLysAsnCys 100
Db 364 CCTTTGAACCTGGAACATATCAATCTAGTTGTTATTTTCTTCTACGACAACTTGACC 423
QY 101 TrpSerSerLeuLeuLysAsnCysSerAspMetGlyAlaHisLeuValValIleAspThr 120
Db 424 TGGTCATCAAGTTTAAAGAAATGCTCAGACATGGGGCTCACCTGGTGGTATCGACACA 483
QY 121 GlnGluGlnGlnPheLeuPheArgThrLysProLysArgLysGluPheTyrlleGly 140
Db 484 CAGGAAGACGAGGAATTCCTTTTCGCACAAAATCTAAAGGAAAGAGCTTTATATTGGA 543
QY 141 LeuThrAspGlnValValGluGlyGlnTrpGlnTrpValAspThrProPheThrGlu 160
Db 544 CTGACAGACCGGTGGTGGAGGTGAGTGGCAATGGGAGGATGATACACCTTTCACAG 603
QY 161 SerLeuSerPheTrpAspAlaGlyGluProAsnAsnIleValLeuValGluAspCysAla 180
Db 604 TCCCTGACCTCTGGGATGCTGGGAGGCCCAACAATATAGTTTGGTGGAGGACTGTGCC 663
QY 181 ThrIleArgAspSerSerAsnSerArgLysAsnTrpAsnAspIleProCysPheTrpSer 200
Db 664 ACCATAAGGAGCTCTTCAAACTCCAGGAAGAACTGGAATGATAATCCCTGTTTCTACAGT 723
QY 201 MetProTrpIleCysGluMetProGluIleSerProLeuAsp 214
Db 724 ATGCCCTTGGATTGTGAGATGCCAGNAATAAGTCTCTCAGGAC 765

RESULT 5
BD094039
LOCUS BD094039 730 bp mRNA linear ROD 12-OCT-2004
DEFINITION Rattus norvegicus macrophage-inducible C-type lectin (Clec3f9)
ACCESSION BD094039
VERSION BD094039.1 GI:38352001
KEYWORDS Rattus norvegicus (Norway rat)
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1. (bases 1 to 730)
Flornes, L.M., Bryceon, Y.T., Spurkland, A., Lorentzen, J.C.,
Dissen, E. and Fossum, S.
Identification of lectin-like receptors expressed by antigen
presenting cells and neutrophils and their mapping to a novel gene
complex
Immunogenetics 56 (7), 506-517 (2004)
2. (bases 1 to 730)
Flornes, L.M., Dissem, E. and Fossum, S.
Direct Submission
Submitted (06-AUG-2003) Anatomy, University of Oslo, PO Box 1105
Blindern, Oslo 0317, Norway
Location/Qualifiers
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1..730
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ORIGIN

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Score: 1049.50 Matches: 190
Percent Similarity: 93.49% Conserved: 11
Best Local Similarity: 88.37% Mismatches: 13
Query Match: 89.02% Indels: 1
DB: 10 Gaps: 1

US-10-812-620-2 (1-214) x AY363175 (1-730)

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Db 111 CAAGTGCTTCATGGACGATGGCTGGGCGCTCCATCGTCTCAGTGCTGTTCATC 170
Qy 41 ThrArgCysValValThrTyArgSerSerGlnIleSerGlyGln---AsnLeuGlnPro 59
Db 171 ACCAGATGCTGTTGAACATATACAGTCTTTCAAAATTTATGGCAGAGAGATTACAGCCA 230
Qy 60 HisArgAsnIleLysGluLeuSerCysTyIleSerGluAlaSerGlySerValLysAsnCys 79
Db 231 CATAAACTATTAGGAGCTTCTCTGCTACCTTGAAGCATCAGGTTCAGTCAAGAAATGC 290
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Db 291 TGCCTTTGAAGTGAACATTTTCAGTCTAGTGTCTACTTTTCTACAAACACCTTA 350
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Db 531 GAGTCCCTGAGCTTCTGGATGCTGGAGAGCCCAATACATAGTTTTTGTGGAGGACTGT 590
Qy 180 AlaThrIleArgAspSerSerAsnSerArgLysAsnTrpAsnAspIleProCysPheTyI 199
Db 591 GCCACCATGAGGGACTCTTCAAAACCCAGGAAGAACTGGAATGATGATCCTGTTCTTC 650
Qy 200 SerMetProTrpIleCysGluMetProGluIleSerProLeuAsp 214
Db 651 AGTATGCTTGATTTGTGAGATGCCAGAAATAAGTCTCTTGGAC 695

RESULT 6

BC000715 927 bp mRNA linear PRI 29-JUN-2004
LOCUS
DEFINITION Homo sapiens C-type (calcium dependent, carbohydrate-recognition domain) lectin, superfamily member 9, mRNA (cDNA clone MGC:1246 IMAGE:3507103), complete cds.
ACCESSION BC000715
VERSION BC000715.2 GI:33875777
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 927)
Krausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Narusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Schetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Boak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shrivchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalek, U., Smillie, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 927)
Krausberg, R.
Direct Submission
Submitted (15-NOV-2000) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
On Aug 19, 2003 this sequence version replaced gi:12653848.
Contact: MGC help desk
Email: cgapba-t@mail.nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library Preparation: Rubin Laboratory
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbio.org>
contact: amadon@systemsbio.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha
Madan, Stephanie Rodriguez, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAL Plate: 7 Row: 1 Column: 14
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 7657332.

FEATURES

Location/Qualifiers
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gene

CDS

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DB:		9		6		2			
US-10-812-620-2 (1-214) x BC000715 (1-927)									
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Qy	41	ThrArgCysValValThrTyArgSerSerGlnIleSerGlyGln---	59						
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Db	261	CCTGAGAATTTACAGAGCTCTCTGCTACAATATATGGATCAGGTTTCAGTCAAGAAATGT	320						
Qy	80	CysProLeuAsnTrpLysHisTyGlnSerSerCysTySerPhePheSerThrThrThrLeu	99						
Db	321	TGTCCATTGAACCTGGGAATATTTTCAATCCAGCTGCTACTTCTTTCTACTGACACCAT	380						
Qy	100	ThrTrpSerSerSerLeuLysAsnCysSerAspMetGlyAlaHisLeuValValleAsp	119						
Db	381	TCCTGGCGCTTAAGTTTAAAGAACTGCTCAGCCATGGGGGCTCACCTGGTGGTTATCAAC	440						
Qy	120	ThrGlnGluGluGlnGluPheLeuPheArgThrLysProLysArgLysGluPheTyrlle	139						
Db	441	TCACAGGAGGACAGGAATCTTCTTCTACAGAAACCTTAAATGAGAGTTTTTTATT	500						
Qy	140	GlyLeuThrAspGlnValValGluGlyGlnTrpGlnTrpValAspThrProPheThr	159						
Db	501	GGACTGTACAGACAGGTTGTCAGGGTTCAGTGGCAATGGTGGCGCACACCTTTGACA	560						
Qy	160	GluSerLeuSerPheTrpAspIleGlyGluProAsnAsnIleValLeuValGluAspCys	179						
Db	561	AAGTCTCTGAGCTTCTGGGATGTAGGGGAGCCCAACACATAGCTACCTGGAGGACTGT	620						
Qy	180	AlaThrIleArgAspSerSerAsnSerArgLysAsnTrpAsnAspIleProCysPheTyrl	199						
Db	621	GCCACCATGAGAGACTCTTCAAACCCCAAGGCAAAATTTGGAATGATGTAACCTGTTTCCTC	680						
Qy	200	SerMetProTrpIleCysGluMetProGluIleSerProLeuAsp	214						
Db	681	AATTATTTTCGGATTGTTGAATGGTAGGAATAAATCTTTTGAC	725						
RESULT 7									
AX083498		968 bp		DNA		linear		PAT 28-FEB-2001	
LOCUS		Sequence 40 from Patent WO0112662.							
DEFINITION									
ACCESSION		AX083498							
VERSION		AX083498.1		GI:13185308					
KEYWORDS		Homo sapiens (human)							
SOURCE		Homo sapiens							
ORGANISM		Homo sapiens							
REFERENCE		1							
AUTHORS		Lal, P., Yue, H., Tang, Y.T., Bandman, O., Burford, N., Azimzai, Y.,							
TITLE		Baughn, M.R., Lu, D.A. and Patterson, C.							
JOURNAL		Membrane associated proteins							
		Patent: WO 0112662-A 40 22-FEB-2001;							
US-10-812-620-2 (1-214) x AX083498 (1-968)									
Qy	1	MetAsnSerThrLysSerProAlaSerHisHisThrGluArgGlyCysPheLysAsnSer	20						
Db	162	ATGAATTCATCTAAATCATCTGAAACACAACTGACACAGAGAGGATGCTTC	218						
Qy	21	GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPhele	40						
Db	219	CAAAATGTTCTTATGGACTGTTGCTGGATCCCATCTATTTCTCAGTGCCTGTTTCATC	278						
Qy	41	ThrArgCysValValThrTyArgSerSerGlnIleSerGlyGln---	59						
Db	279	ACCAGATGTTGTGACATTTTCCATCTTTCAAACCTGTGATGAGAAAAAGTTTCAGCTA	338						
Qy	60	HisArgAsnIleLysGluLeuSerCysTySerGluAlaSerGlySerValLysAsnCys	79						
Db	339	CCTGAGAATTTACAGAGCTCTCTGCTACAATATATGGATCAGGTTTCAGTCAAGAAATGT	398						
Qy	80	CysProLeuAsnTrpLysHisTyGlnSerSerCysTySerPhePheSerThrThrThrLeu	99						
Db	399	TGTCCATTGAACCTGGGAATATTTTCAATCCAGCTGCTACTTCTTTCTACTGACACCAT	458						
Qy	100	ThrTrpSerSerSerLeuLysAsnCysSerAspMetGlyAlaHisLeuValValleAsp	119						
Db	459	TCCTGGCGCTTAAGTTTAAAGAACTGCTCAGCCATGGGGGCTCACCTGGTGGTTATCAAC	518						
Qy	120	ThrGlnGluGluGlnGluPheLeuPheArgThrLysProLysArgLysGluPheTyrlle	139						
Db	519	TCACAGGAGGACAGGAATTCCTTCTTCTACAGAAACCTTAAATGAGAGTTTTTTATT	578						
Qy	140	GlyLeuThrAspGlnValValGluGlyGlnTrpGlnTrpValAspThrProPheThr	159						
Db	579	GGACTGTACAGACAGGTTGTCAGGGTTCAGTGGCAATGGTGGCGCACACCTTTGACA	638						
Qy	160	GluSerLeuSerPheTrpAspIleGlyGluProAsnAsnIleValLeuValGluAspCys	179						
Db	639	AAGTCTCTGAGCTTCTGGGATGTAGGGGAGCCCAACACATAGCTACCTGGAGGACTGT	698						
Qy	180	AlaThrIleArgAspSerSerAsnSerArgLysAsnTrpAsnAspIleProCysPheTyrl	199						
Db	699	GCCACCATGAGAGACTCTTCAAACCCCAAGGCAAAATTTGGAATGATGTAACCTGTTTCCTC	758						
Qy	200	SerMetProTrpIleCysGluMetProGluIleSerProLeuAsp	214						
Db	759	AATTATTTTCGGATTGTTGAATGGTAGGAATAAATCTTTTGAC	803						
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LOCUS		Secreted and transmembrane polypeptides and nucleic acids encoding							
DEFINITION		the same.							
ACCESSION		BD172543							
VERSION		BD172543.1		GI:28413845					
KEYWORDS		JP 200223786-A/316.							
SOURCE		Homo sapiens (human)							
ORGANISM		Homo sapiens							

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 997)
Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and
Yuan,J.
Secreted and transmembrane polypeptides and nucleic acids encoding
the same

REFERENCE
AUTHORS

TITLE

JOURNAL Patent: JP 2002223786-A 316 13-AUG-2002;

COMMENT

GENENTECH INC
OS Homo sapiens (human)
PN JP 2002223786-A/316
PD 13-AUG-2002 JP 2001385135

PF 18-DEC-2001 JP 2001385135 60/059115,17-SEP-1997 US 60/059184 PR
PR 17-SEP-1997 US 60/059122,17-SEP-1997 US 60/059117 PR

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17-SEP-1997 US 60/059119,18-SEP-1997 US 60/059263 PR

18-SEP-1997 US 60/059266,15-OCT-1997 US 60/062125 PR
17-OCT-1997 US 60/062287,17-OCT-1997 US 60/062285 PR

21-OCT-1997 US 60/063486,24-OCT-1997 US 60/062816 PR
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28-OCT-1997 US 60/063549,28-OCT-1997 US 60/063541 PR

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29-OCT-1997 US 60/063734,29-OCT-1997 US 60/063738 PR
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07-NOV-1997 US 60/064809,12-NOV-1997 US 60/065186 PR

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21-NOV-1997 US 60/066120,21-NOV-1997 US 60/066364 PR

24-NOV-1997 US 60/066772,24-NOV-1997 US 60/066466 PR
24-NOV-1997 US 60/066770,24-NOV-1997 US 60/066511 PR

24-NOV-1997 US 60/066453,25-NOV-1997 US 60/066840 PI
WILLIAM I WOOD, AUSTIN L GURNEY, AUDREY GODDARD, DIANE PENNICA, PI
JIAN ZHENG,

PI JEAN YUAN
PC C12N15/09, C07K14/47, C07K16/18, C07K19/00, C12N1/19, C12N1/21, PC
C12N5/10,

PC C12P21/02, C12P21/08, (C12P21/02, C12R1:19), (C12P21/02, C12R1:91), PC
(C12P21/02, C12R1:645), C12N15/00, C12N5/00

CC Secreted and transmembrane polypeptides and nucleic CC acids
encoding the same

FH Key

FT source Location/Qualifiers

FT 1..997 /organism='Homo sapiens (human)'.
1..997 /organism='Homo sapiens (human)'.
/mol_type='genomic DNA'
/db_xref='taxon:9606'

FEATURES
source

ORIGIN

Alignment Scores:

Pred. No.: 8.18e-70 Length: 997
Score: 774.00 Matches: 143
Percent Similarity: 79.07% Conservative: 27
Best Local Similarity: 66.51% Mismatches: 43
Query Match: 65.65% Indels: 2
DB: 6 Gaps: 2

US-10-812-620-2 (1-214) x BD172543 (1-997)

Qy 1 MetAenSerThrLysSerProAlaSerHisThrGluArgGlyCysPheLysAenSer 20

Db 106 ATGAAATCATCTAAATCATCTGAAACAATATGCACAGAGAGAGTCTTC---TCTTCC 162

Qy 21 GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle 40

Db 163 CAATGTTCTTATGGAGCTGTGTGGATCCCATCTTATTTCTCAGTGCCTGTTTCATC 222
Qy 41 ThrArgCysValValThrTyrArgSerSerGlyGln---AenLeuGlnPro 59
Db 223 ACCAGATGTTGTGACATTTCCGATCTTTCAACCTGTGATGAGAAAAGTTTCAGCTA 282
Qy 60 HisArgAenIleLysGluLeuSerCysTyrSerGluAlaSerGlySerValLysAenCys 79
Db 283 CCTGAGAAATTTACAGAGCTCTCTCTGCTACAATATATGGATCAGGTTTCAAGAAATGT 342
Qy 80 CysProLeuAenTrpLysHisTyrGlnSerSerCysTyrPhePheSerThrThrLeu 99
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Qy 100 ThrTrpSerSerSerLeuLysAenCysSerAspMetGlyAlaHisLeuValLysAen 119
Db 403 TCTGGCGTTAAGTTTAAAGAACTGCTCAGCCATGGGGGCTCACCTGGTGGTTATCAAC 462
Qy 120 ThrGlnGluGlnGluPheLeuPheArgThrLysProLysArgLysGluPheTyrIle 139
Db 463 TCACAGGAGGAGCAGGAATTTCTTCTCACAAGAAACCTAAATGACAGAGATTTTATT 522
Qy 140 GlyLeuThrAspGlnValGluGlyGlnTrpGlnTrpValAspAspThrProPheThr 159
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Qy 160 GluSerLeuSerPheTrpAspAlaGlyGluProAenAenIleValLeuValGluAspCys 179
Db 583 AAGTCTCTGAGCTTCTGGGATGTAGGGAGGCCAACCAACATAGCTACCTGGAGGACTGT 642
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Qy 200 SerMetProTrpIleCysGluMetProGluIleSerProLeuAen 214
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RESULT 9

BD172862

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BD172862 997 bp DNA linear PAT 18-FEB-2003
Secreted and transmembrane polypeptides and nucleic acids encoding
the same.

BD172862 1 GI:28414166

JP 200238586-A/316.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 997)

Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and

Yuan,J.

Secreted and transmembrane polypeptides and nucleic acids encoding

the same

Patent: JP 2002238586-A 316 27-AUG-2002;

GENENTECH INC

OS Homo sapiens (human)

PN JP 2002238586-A/316

PD 27-AUG-2002

PF 18-DEC-2001 JP 2001385205

PR 17-SEP-1997 US 60/059115,17-SEP-1997 US 60/059184 PR

17-SEP-1997 US 60/059122,17-SEP-1997 US 60/059117 PR

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18-SEP-1997 US 60/059266,15-OCT-1997 US 60/062125 PR

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24-NOV-1997 US 60/066453, 25-NOV-1997 US 60/066840 PI
WILLIAM I WOOD, AUSTIN L GURNEY, AUDREY GODDARD, DIANE PENNICA, PI
JIAN ZHENG,
PI JEAN YUAN
PC C12N15/09, C07K14/47, C07K16/18, C07K19/00, C12N1/19, C12N1/21, PC
C12N5/10.
PC C12P21/02//C12P21/08, (C12N1/19, C12R1:645), (C12N1/21, C12R1:19),
PC (C12N5/10, C12R1:91), (C12P21/02, C12R1:91), (C12P21/02, C12R1:645), PC
(C12P21/02, C12R1:19), (C12P21/08, C12R1:91), C12N15/00, C12N5/00, PC
(C12N5/00, C12R1:91)
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encoding the same
FH Key Location/Qualifiers
FT source 1. 997
/organism="Homo sapiens (human)".
/organism="Homo sapiens"
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FEATURES

source

ORIGIN

Alignment Scores:
Pred. No.: 8,18e-70 Length: 997
Score: 774.00 Matches: 143
Percent Similarity: 79.07% Conservative: 27
Best Local Similarity: 66.51% Mismatches: 43
Query Match: 65.65% Indels: 2
DB: 6 Gaps: 2
US-10-812-620-2 (1-214) x BD172862 (1-997)
QY 1 MetAsnSerThrLysSerProAlaSerHisHisThrGluArgGlyCysPheLysAsnSer 20
DB 106 ATGAATTCATCTAAATCATCTGAAACACAATGCACAGAGAGGATGCTTC---TCTTCC 162
QY 21 GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle 40
DB 163 CAATATGTTCTTATGGACTGTTGCTGGGATCCCATCTCTATTTCTCAGTGCCTGTTTCATC 222
QY 41 ThrArgCysValValThrTrpArgSerSerGlnIleSerGlyGln---AsnLeuGlnPro 59
DB 223 ACCAGATGTTGTGTGACATTCGCATCTTTCAACCTGTGATGAGAAAAGTTTCAGCTA 282
QY 60 HisArgAsnIleLysGluLeuSerCysTrpSerGluAlaSerGlySerValLysAsnCys 79
DB 283 CCTGAGAATTCACAGAGCTCTCTGCTACAAATATGATGAGTTCAGTCAAGAATTC 342
QY 80 CysProLeuAsnTrpLysHisTrpGlnSerSerCysTrpPhePheSerThrThrLeu 99
DB 343 TGTCCATTGAACCTGGGAATTTTCAATCCAGCTGCTACTTCTTTCTACTGACACCACT 402
QY 100 ThrTrpSerSerLeuLysAsnCysSerAspMetGlyAlaHisLeuValIleAsp 119
DB 403 TCTGGGCGTTAAGTTTAAGAACTCTCAGCCATGGGGGCTCACCCTGTGGTTATCAAC 462
QY 120 ThrGlnGluGlnGluPheLeuPheArgThrLysProLysArgLysGluPheTrpIle 139
DB 463 TCACAGGAGGAGCAGGAATTCCTTTCTCACAAGAAACCTTAAATATGAGAGAGTTTTTATT 522

QY 140 GlyLeuThrAspGlnValValGluCluGlyGlnTrpGlnTrpValAspAspThrProPheThr 159
DB 523 GGACGTGTGACACAGGTTGTGAGGGTCAGTGGCAATGGGTGACGGACACACCTTTTGACA 582
QY 160 GluSerLeuSerPheTrpAspAlaGlyGluProAsnAsnIleValLeuValGluAspCys 179
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QY 180 AlaThrIleArgAspSerSerAsnSerArgLysAsnTrpAsnAspIleProCysPheTrp 199
DB 643 GCCACCATGAGAGACTCTTCAAAACCAAGGCAAAATTCGAATGATGTAACCTGTTTCTC 702
QY 200 SerMetProTrpIleCysGluMetProGluLeuSerProLeuAsp 214
DB 703 AATTATTTTCGATTTGTGAAATGTTAGGAATAAATCTCTTTGAAC 747
RESULT 10
BD173181
LOCUS
DEFINITION
Secreted and transmembrane polypeptides and nucleic acids encoding
the same.
ACCESSION
BD173181
VERSION
BD173181.1 GI:28414490
KEYWORDS
JP 2002238587-A/316.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 997)
AUTHORS
Wood, W.I., Gurney, A.L., Goddard, A., Pennica, D., Zheng, J. and
Yuan, J.
TITLE
Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL
Patent: JP 2002238587-A 316 27-AUG-2002;
GENENTECH INC
COMMENT
OS Homo sapiens (human)
PN JP 2002238587-A/316
PD 27-AUG-2002
PF 18-DEC-2001 JP 2001385248
PR 17-SEP-1997 US 60/059115, 17-SEP-1997 US 60/059184 PR
17-SEP-1997 US 60/059122, 17-SEP-1997 US 60/059121 PR
17-SEP-1997 US 60/059113, 17-SEP-1997 US 60/059263 PR
17-SEP-1997 US 60/059119, 18-SEP-1997 US 60/062125 PR
18-SEP-1997 US 60/059266, 15-OCT-1997 US 60/062285 PR
17-OCT-1997 US 60/062287, 17-OCT-1997 US 60/062816 PR
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24-NOV-1997 US 60/066453, 25-NOV-1997 US 60/066840 PI
WILLIAM I WOOD, AUSTIN L GURNEY, AUDREY GODDARD, DIANE PENNICA, PI
JIAN ZHENG,
PI JEAN YUAN
PC C12N15/09, C07K14/47, C07K16/18, C12N1/19, C12N1/21, C12N5/10, PC
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and transmembrane polypeptides and nucleic CC acids encoding the same

Key Location/Qualifiers

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Location/Qualifiers

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ORIGIN

Alignment Scores:

Pred. No.: 8.18e-70 Length: 997

Score: 774.00 Matches: 143

Percent Similarity: 79.07% Conservative: 27

Best Local Similarity: 66.51% Mismatches: 43

Query Match: 65.65% Indels: 2

DB: 6 Gaps: 2

US-10-812-620-2 (1-214) x BD173181 (1-997)

Qy 1 MetAsnSerThrIysSerProAlaSerHisThrGluArgGlyCysPheLysAsnSer 20

Db 106 ATGAATTCATCTAAATCATCTGAAACACAATGCACAGAGAGGATGCTTC---TCTTCC 162

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Qy 60 HisArgSerIleLysGluLeuSerCysTrpSerGluAlaSerGlySerValLysAsnCys 79

Db 283 CCTGAGAATTTTCAGAGAGCTCTCTGCTACAAATTTATGATGATGATGATGATGATGAT 342

Qy 80 CysProLeuSerTrpLysHisThrGlnSerSerCysTrpPhePheSerThrThrThrLeu 99

Db 343 TGTCCATTTGAATGGGAATATTTTCAATCCAGCTGCTACTTCTTCTTCTGACCACTT 402

Qy 100 ThrTrpSerSerLeuLysAsnCysSerAspMetGlyAlaHisLeuValValIleAsp 119

Db 403 TCTCTGGGCGTTAAGTTAAAGAACTGTCTACCCATGGGGCTCCTGCTGGTATCAAC 462

Qy 120 ThrGlnGluGlnGlnGluPheLeuPheArgThrLysProLysArgLysGluPheTyrlle 139

Db 463 TCACAGGAGGACGAGGAATTCCTTTCTTCAAGAAACCTAAATGACAGAGAGTTCCTTAT 522

Qy 140 GlyLeuThrAspGlnValValGluGlyGlnTrpGlnTrpValAspAspThrProPheThr 159

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Qy 160 GluSerLeuSerPheTrpAspAlaGlyCyluProAsnAsnIleValLeuValGluAspCys 179

Db 583 AAGTCTCTGAGCTCTGGGATGTAGGGAGGCCAACACATAGTACCTGGAGAGATGT 642

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RESULT 11

BD173500

LOCUS

BD173500 997 bp DNA linear PAT 18-FEB-2003

DEFINITION

Secreted and transmembrane polypeptides and nucleic acids encoding the same.

ACCESSION

BD173500

VERSION

BD173500.1 GI:28414831

KEYWORDS

JP 2002238588-A/316.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 997)

AUTHORS

Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and Yuan,J.

TITLE

Secreted and transmembrane polypeptides and nucleic acids encoding the same

JOURNAL

Patent: JP 2002238588-A 316 27-AUG-2002;

COMMENT

GENENTECH INC

OS Homo sapiens (human)

PN JP 2002238588-A/316

PD 27-AUG-2002

PF 18-DEC-2001 JP 2001385315

PR 17-SEP-1997 US 60/059115, 17-SEP-1997 US 60/059184 PR

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WILLIAM I WOOD, AUSTIN L GURNEY, AUDREY GODDARD, DIANE PENNICA, PI

JIAN ZHENG,

PI JEAN YUAN

PC C12N15/09, C07K16/435, C07K19/00, C12N1/19, C12N1/21, PC

C12N5/10,

PC C12P21/02//C12P21/08, (C12N1/19, C12R1.645), (C12N1/21, C12R1.19),

PC (C12N5/10, C12R1.91), C12N15/00, C12N5/00, (C12N5/00, C12R1.91) CC

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FT Key Location/Qualifiers

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Location/Qualifiers

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source

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Alignment Scores:

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Score: 774.00 Matches: 143

Percent Similarity: 79.07% Conservative: 27

Best Local Similarity: 66.51% Mismatches: 43

Query Match: 65.65% Indels: 2

DB: 6 Gaps: 2

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KEYWORDS  JP 2002253280-A/316.
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ORGANISM  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 997)
AUTHORS   Wood,W.I., Gurney,A.L., Goddard,A., Pennica,D., Zheng,J. and
Yuan,J.
TITLE      Secretory and transmembrane polypeptide and nucleic acid encoding
the same
JOURNAL   Patent: JP 2002253280-A 316 10-SEP-2002;
GENENTECH INC
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PN JP 2002253280-A/316
PD 10-SEP-2002
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24-NOV-1997 US 60/066453,25-NOV-1997 US 60/066840 PI
WILLIAM I WOOD,AUSTIN L GURNEY,AUDREY GODDARD,DIANE PENNICA, PI
JIAN ZHENG,
PI JEAN YUAN
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Secretory and transmembrane polypeptide and nucleic acid CC
encoding the same
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1..997
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Pred. No.: 8,18e-70 Length: 997
Score: 774.00 Matches: 143
Percent Similarity: 79.07% Conservative: 27
Best Local Similarity: 66.51% Mismatches: 43
Query Match: 65.65% Indels: 2
DB: 6 Gaps: 2
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QY 21 GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle 40
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DEFINITION Sequence 376 from patent US 6686451.
ACCESSION AR473298
VERSION AR473298.1 GI:42708673
KEYWORDS
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REFERENCE
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Williams,P.M. and Wood,W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: US 6686451-A 376 03-FEB-2004;
FEATURES
Location/Qualifiers
1..997
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ORIGIN

Alignment Scores:
Pred. No.: 8,18e-70 Length: 997
Score: 774.00 Matches: 143
Percent Similarity: 79.07% Conservative: 27
Best Local Similarity: 66.51% Mismatches: 43
Query Match: 65.65% Indels: 2
DB: 6 Gaps: 2

US-10-812-620-2 (1-214) x AR473298 (1-997)

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Db     283  CCGAGAAATTCACAGAGCTCTCTCTCTACAATATGGATCAGGTTTCAGTCAAGAAATGT  342

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Search completed: June 9, 2005, 15:27:36

Job time : 4161 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 9, 2005, 09:39:25 ; Search time 531 Seconds
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Listing first 45 summaries

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5	774	65.6	997	2 AAX52274	Aax52274 Protein p

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DT 23-JUL-2001 (first entry)
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KW Mouse; Mincle; C-type lectin; antiinflammatory; macrophage; inflammation;
KW immune disorder; nuclear factor interleukin 6; NF-IL6; ss.
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FT /note= "C-type lectin"
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DF 02-OCT-2000; 2000WO-JP006820.
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PR 15-OCT-1999; 99JP-00293724.
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PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX Akira S, Matsumoto M;
XX WPI; 2001-273771/28.
DR P-PSDB; AAB97225.
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PT New macrophage activating C-type lectin for the treatment of immune
PT disorders and inflammation.
XX
XX
PS Claim 4; Fig 4; 60pp; Japanese.
XX
XX This invention relates to a C-type lectin, termed Mincle, which is formed
CC from a transcriptional target gene of nuclear factor interleukin 6 (NF-
CC IL6). Mincle is a macrophage activating protein which can be used in the
CC treatment of immune disorders, and inflammation. Compositions containing
CC the protein have immunomodulatory and antiinflammatory activity. The
CC present sequence represents murine cdna encoding Mincle
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Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-10-812-620-2 (1-214) x AAF86349 (1-2517)

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DB 184 CAAGTGTCTCTCGACAGATACCGGGGCTCCATCTGTTCTCAGTGGCTGTTTCATC 243

QY 41 ThrArgCysValValThrTyrArgSerSerGlnIleSerGlyGlnAsnLeuGlnProHis 60
DB 244 ACCAGATGTGCTTAACATATGCAGCTCTCAAAATTCGGGGCAGAACTTACAGCCACAT 303

QY 61 ArgAsnIleGlyGluLeuSerCysTyrSerGluAlaSerClySerValLysAsnCysCys 80
DB 304 AGAAATATTAAAGAGCTTTCCTGCTACAGTGAGGCATCAGGTTCAAGAAATTGCTGT 363

QY 81 ProLeuAsnTrpLysHisTyrGlnSerSerCysTyrPhePheSerThrThrLeuThr 100
DB 364 CTTTGAACCTGGAACATTTATCATCTAGTTGTTATTTTCTTACGACAACTTGACC 423

QY 101 TrpSerSerSerLeuLysAsnCysSerAspMetGlyAlaHisLeuValValIleAspThr 120
DB 424 TGGTCATCAAGTTTAAAGAAATGCTCAGACATGGGGGCTCACCTGGTGGTTATCGACACA 483

QY 121 GlnGluGluGlnGluPheLeuPheArgThrLysProLysArgLysGluPheThrIleGly 140
DB 484 CAGGAAGACGACGAAATCTCTTTTCGCACAAAACCTTAAAGAAAGAGTTTATATTGA 543

QY 141 LeuThrAspGlnValValGluGlyGlnTrpGlnTrpValAspAspThrProPheThrGlu 160
DB 544 CTGACAGACAGAGTGTGGAGGTGCTAGTGGCAATGGGTGGATGATACACTTTCACAGAG 603

QY 161 SerLeuSerPheTrpAspAlaGlyGluProAsnAsnIleValLeuValGluAspCysAla 180
DB 604 TCCCTGAGCTTCTGGGATGCTGGGGAGCCCAACAATATAGTTTGGTGGAGGACTGTGCC 663

QY 181 ThrIleArgAspSerSerAsnSerArgLysAsnTrpAsnAspIleProCysPheThrSer 200
DB 664 ACCATAAGGGACTCTTCAAACTCCAGGAAGAACTGGAATGATATACCTGTTTCTACAGT 723

QY 201 MetProTrpIleCysGluMetProGluIleSerProLeuAsp 214
DB |||||

Db 724 ATGCCTTGGATTGTGAGATGCCAGAAATAAGTCTCTCTGGAC 765
RESULT 2
AAF81743
ID AAF81743 standard; cDNA; 968 BP.
XX
AC AAF81743;
XX
DT 12-JUN-2001 (first entry)
XX
DE Human membrane associated protein MEMAP-3 encoding cDNA.
XX
KW Human; membrane associated protein; MEMAP; diagnosis; cytostatic;
KW antiinflammatory; anticonvulsant; immunosuppressive; antidiarrheic;
KW antiarteriosclerotic; gene therapy; cell proliferative disorder;
KW autoimmune disorder; inflammatory disorder; neurological disorder;
KW gastrointestinal disorder; cancer; inflammation; atherosclerosis;
KW epilepsy; diarrhoea; ss.
XX
OS Homo sapiens.
XX
PN WO200112662-A2.
XX
PD 22-FEB-2001.
XX
PF 14-AUG-2000; 2000WO-US022315.
XX
PR 17-AUG-1999; 99US-0149641P.
PR 09-NOV-1999; 99US-0164203P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Lal P, Yue H, Tang YT, Bandman O, Burford N, Azimzai Y;
PI Baughn MR, Lu DAM, Patterson C;
XX
WPI; 2001-168860/17.
DR P-PSDB; AAB74697.
XX
PT Isolated polypeptide with a human membrane associated protein sequence is
PT useful for the diagnosis, prevention and treatment of cell proliferative,
PT autoimmune/inflammatory, neurological and gastrointestinal disorders.
XX
PS Example; Page 151; 173pp; English.
XX
CC AAF81741 to AAF81777 encode the human membrane associated proteins
CC (MEMAP) given in AAB74695 to AAB74731. MEMAPs have cytostatic,
CC antiinflammatory, anticonvulsant, immunosuppressive, antidiarrheic and
CC antiarteriosclerotic activities, which can be used in gene therapy.
CC MEMAPs and agonist of MEMAPs can be used to treat a disease or condition
CC associated with decreased expression of functional MEMAP and antagonists
CC of MEMAP are used to treat a disease or condition associated with
CC overexpression of functional MEMAP. These disorders include cell
CC proliferative, autoimmune/inflammatory, neurological and gastrointestinal
CC disorders. The MEMAP polynucleotides and proteins are also used for the
CC diagnosis of these disorders. Specific examples of these disorders
CC include cancer, inflammation, atherosclerosis, epilepsy and diarrhoea.
CC MEMAP proteins can be used to screen for compounds which specifically
CC bind MEMAP including antibodies, oligonucleotides, proteins and small
CC molecules. MEMAP polynucleotides can be used to prepare transgenic
CC animals which can be studied to provide information concerning human
CC disease. Anti-MEMAP antibodies are useful in immunoassays for the
CC detection of MEMAP protein and can be used as antagonists to treat or
CC prevent a disorder associated with MEMAP. Polynucleotides encoding MEMAP
CC can be delivered to target cells with genetic abnormalities with respect
CC to the expression of MEMAP to treat or prevent a disorder associated with
CC MEMAP
XX
SQ Sequence 968 BP; 314 A; 197 C; 205 G; 252 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.35e-72 Length: 968
Score: 774.00 Matches: 143
Percent Similarity: 79.07% Conservative: 27


```

RESULT 4
ADRA1300
ID ADRA1300 standard; cDNA; 990 BP.
AC ADRA1300;
XX
DT 07-OCT-2004 (first entry)
XX
DE Human CD-like molecule HYAM43 cDNA, SEQ ID NO:99.
XX
KW Human; CD-like molecule; cluster of differentiation; diagnosis;
KW prevention; immune disorder; immunodeficiency; autoimmune disorder;
KW blood-related disorder; haematological disorder; haemostatic disorder;
KW thrombolytic disorder; hyperproliferative disorder; cancer; tumour;
KW apocytic disorder; cardiovascular disorder; respiratory disorder;
KW angogenic disorder; neovascularisation; neurological disorder;
KW endocrine disorder; reproductive system disorder; infectious disease;
KW gastrointestinal disorder; drug screening; tissue regeneration;
KW chemotaxis; gene therapy; antibody therapy; drug targeting;
KW chromosome mapping; forensic analysis; immunophenotyping; cytostatic;
KW haemostatic; tranquiliser; vulnerary; anti-inflammatory; nephrotropic;
KW cardiac; antiallergic; anti-HIV; antirheumatic; antiarthritic;
KW antipsoriatic; immunosuppressive; vasotropic; neutropic; neuroprotective;
KW antithyroid; thyromimetic; gynaecological; virucide; hepatotropic;
KW antibacterial; dermatological; gene; ss.
XX
OS Homo sapiens.
XX
XX WO200226930-A2.
XX
XX 04-APR-2002.
XX
XX 25-SEP-2001; 2001WO-US029838.
XX
XX 26-SEP-2000; 2000US-0235484P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Birse CE;
XX
XX WPI; 2002-405050/43.
XX
XX P-PSDB; ADRA1476.
XX
XX Novel polynucleotides and polypeptides useful for treating, preventing or
XX ameliorating cardiovascular, renal, neurovascular, and autoimmune
XX disorders.
XX
XX Claim 4; SEQ ID NO 99; 1243pp; English.
XX
XX The invention relates to 167 novel human CD (cluster of differentiation)-
XX like molecules (ADRA1388-ADRA1563) and to cDNAs encoding them (seqid:1)-
XX
XX Sequence 990 BP; 342 A; 192 C; 206 G; 249 T; 0 U; 1 Other;
XX
Alignment Scores:
Pred. No.: 1,39e-72 Length: 990
Score: 774.00 Matches: 143
Percent Similarity: 79.07% Conservative: 27
Best Local Similarity: 66.51% Mismatches: 43
Query Match: 65.65% Indels: 2
DB: 7 Gaps: 2
US-10-812-620-2 (1-214) x ADRA1300 (1-990)
QY 1 MetAsnSerThrIysSerProAlaSerHisHisThrGluArgGlyCysPheIysAenSer 20
Db 149 ATGAATTCATCTAAATCACTCTGAAACACATGACACAGAGAGAGATGCTTC---TCTTCC 205
QY 21 GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle 40
Db 206 CAAATGTTCTTATGGACTGTGTGTCGGATCCCATCTATTTCTCAGTCCCTGTTTCATC 265
QY 41 ThrArgCysValValThrTrpTyrArgSerSerGlnIleSerGlyGln---AsnLeuGlnPro 59
Db 266 ACCAGATGCTGTGTGACATTTCCGATCTTTCAAACCTGTGATGAGAAAAAGTTTCAGCTA 325
QY 60 HisArgAenIleLysGluLeuSerCysTyrSerGluAlaSerGlySerValIysAenCys 79
Db 326 CTTGAGAATTTTCACAGAGCTCTCTCTGTCTACAAATATTATGATCAGGTTTCAGTCAAGAATTGT 385
QY 80 CysProLeuAenTrpLysHisTyrGlnSerSerCysTyrPhePheSerThrThrThrLeu 99
Db 386 TGTCCATTGAATCTGGGAATATTTCATCCAGCTGTACTTCTTTTCTACTGACCACTT 445
QY 100 ThrTrpSerSerLeuLysAenCysSerAepMetGlyAlaHisLeuValIleAep 119
Db 446 TCTCTGGGGTTAAGTTTAAAGAACTGCTCAGCCATGGGGGCTCACCCTGGTGTATCAAC 505
QY 120 ThrGlnGluGlnGlnPheLeuPheArgThrLysProLysArgLysGluPheTyrIle 139
Db 506 TCACAGGAGGAGCAGGAATTCCTTCTCTACAAGAAACCTAAATGAGAGAGTTTTTATT 565
QY 140 GlyLeuThrAepGlnValValGluGlyGlnTrpGlnTrpValAepAepThrProPheThr 159
Db 566 GGACTGTGAGACCCAGGTTGTGAGGGTCAGTGGCAATGGTGGAGCGGACACCTTTTGACA 625
QY 160 GluSerLeuSerPheTrpAspAlaGlyGluProAenAenIleValLeuValGluAepCys 179
Db 626 AAGTCTCTGAGCTCTGGGATGTAGGGGAGCCCAACACATAGCTACCTCGGAGGACTGT 685
QY 180 AlaThrIleArgAepSerSerAenSerArgLysAenTrpAenAepIleProCysPheTyr 199
Db 686 GCCACCATGAGAGACTCTTCAACCCAAAGGCAAAATTTGGAATGATGTAACCTGTTTCCTC 745
QY 200 SerMetProTrpIleCysGluMetProGluLeuSerProLeuAep 214
Db 746 AATTATTTTCGATTTGTGAAATGTTAGGAATAAATCTCTTTTGAAC 790
RESULT 5
AAx52274
ID AAx52274 standard; DNA; 997 BP.
XX
XX AAx52274;
XX
XX 25-JUN-1999 (first entry)
XX
XX Protein PRO244 cDNA clone DNA35668-1171.
XX
XX Secreted protein; transmembrane protein; human; enterocolitis;
XX Zollinger-Ellison syndrome; gastrointestinal ulceration;
XX congenital microvillus atrophy; skin disease; cell growth;
XX abnormal keratinocyte differentiation; psoriasis; epithelial cancer;
XX Parkinson's disease; Alzheimer's disease; ALS; neuropathy; fibromodulin;
XX dermal scarring; Usher Syndrome; Atrophia areata; anti-thrombotic;
XX wound healing; tissue repair; ss.
XX
XX Homo sapiens.
XX
XX WO9914328-A2.
XX
XX 25-MAR-1999.
XX
XX 16-SEP-1998; 98WO-US019330.
XX
XX 17-SEP-1997; 97US-0059113P.
XX
XX 17-SEP-1997; 97US-0059113P.
XX
XX 17-SEP-1997; 97US-0059117P.
XX
XX 17-SEP-1997; 97US-0059119P.
XX
XX 17-SEP-1997; 97US-0059121P.
XX
XX 17-SEP-1997; 97US-0059122P.
XX
XX 17-SEP-1997; 97US-0059184P.
XX
XX 18-SEP-1997; 97US-0059263P.
XX
XX 18-SEP-1997; 97US-0059266P.
XX
XX 15-OCT-1997; 97US-0062125P.
XX
XX 17-OCT-1997; 97US-0062285P.

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PR 17-OCT-1997; 97US-0062287P.
 PR 21-OCT-1997; 97US-0063486P.
 PR 24-OCT-1997; 97US-0062814P.
 PR 24-OCT-1997; 97US-0062816P.
 PR 24-OCT-1997; 97US-0063045P.
 PR 24-OCT-1997; 97US-0063120P.
 PR 24-OCT-1997; 97US-0063121P.
 PR 24-OCT-1997; 97US-0063127P.
 PR 24-OCT-1997; 97US-0063128P.
 PR 27-OCT-1997; 97US-0063327P.
 PR 27-OCT-1997; 97US-0063329P.
 PR 27-OCT-1997; 97US-0063541P.
 PR 28-OCT-1997; 97US-0063542P.
 PR 28-OCT-1997; 97US-0063544P.
 PR 28-OCT-1997; 97US-0063549P.
 PR 28-OCT-1997; 97US-0063550P.
 PR 28-OCT-1997; 97US-0063564P.
 PR 29-OCT-1997; 97US-0063435P.
 PR 29-OCT-1997; 97US-0063704P.
 PR 29-OCT-1997; 97US-0063732P.
 PR 29-OCT-1997; 97US-0063734P.
 PR 29-OCT-1997; 97US-0063735P.
 PR 29-OCT-1997; 97US-0063738P.
 PR 29-OCT-1997; 97US-0064215P.
 PR 31-OCT-1997; 97US-0063870P.
 PR 31-OCT-1997; 97US-0064103P.
 PR 03-NOV-1997; 97US-0064248P.
 PR 07-NOV-1997; 97US-0064809P.
 PR 12-NOV-1997; 97US-0065186P.
 PR 17-NOV-1997; 97US-0065846P.
 PR 18-NOV-1997; 97US-0065693P.
 PR 21-NOV-1997; 97US-0066120P.
 PR 21-NOV-1997; 97US-0066364P.
 PR 24-NOV-1997; 97US-0066453P.
 PR 24-NOV-1997; 97US-0066456P.
 PR 24-NOV-1997; 97US-0066511P.
 PR 24-NOV-1997; 97US-0066770P.
 PR 24-NOV-1997; 97US-0066772P.
 PR 25-NOV-1997; 97US-0066840P.
 PR (GETH) GENENTECH INC.
 XX
 XX Wood WI, Gurney AL, Goddard A, Pennica D, Chen J, Yuan J;
 XX WPI; 1999-229533/19.
 DR P-PSDB; AAY13403.
 XX
 PT New isolated human genes and polypeptides used in, e.g. treatment of
 PT Gastrointestinal ulceration.
 XX
 PS Claim 2; Fig 121; 320pp; English.
 XX
 CC AAX52213-74 encode secreted and transmembrane human proteins, and are
 CC obtained from cDNA libraries, prepared from fetal lung, fetal kidney,
 CC fetal brain, fetal liver and fetal retina. The encoded polypeptides have
 CC specific uses based on their homology to known polypeptides, e.g. PRO211
 CC and PRO217 can be used for disorders associated with the preservation and
 CC maintenance of gastrointestinal mucosa and the repair of acute and
 CC chronic mucosal lesions (e.g. enterocolitis, Zollinger-Ellison syndrome,
 CC gastrointestinal ulceration and congenital microvillus atrophy), skin
 CC diseases associated with abnormal keratinocyte differentiation (e.g.
 CC psoriasis, epithelial cancers such as lung squamous cell carcinoma of the
 CC vulva and gliomas), potent effects on cell growth and development,
 CC diseases related to growth or survival of nerve cells including
 CC Parkinson's disease, Alzheimer's disease, ALS, neuropathies or cancer.
 CC PRO265 can be used as for fibromodulin, e.g. for reducing dermal
 CC scarring. PRO264 can be used as a target for anti-tumor drugs. PRO533 may
 CC be used in the treatment of Usher Syndrome or Atrophia areata; PRO269 can
 CC be used as an anti-thrombotic agent; PRO287 polypeptides and portions may
 CC have therapeutic applications in wound healing and tissue repair; PRO317
 CC can be used for treating problems of the kidney, uterus, endometrium,
 CC blood vessels, or related tissue, e.g. in the heart of genital tract
 XX

SQ Sequence 997 BP; 376 A; 189 C; 200 G; 232 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 1,41e-72 Length: 997
 Score: 774.00 Matches: 143
 Percent Similarity: 79.07% Conservative: 27
 Best Local Similarity: 66.51% Mismatches: 43
 Query Match: 65.65% Indels: 2
 DB: Gaps: 2
 US-10-812-620-2 (1-214) x AAX52274 (1-997)
 Qy 1 MetaAenSerThrIysSerProAlaSerHisHisThrGluArgGlyCysPheLysAenSer 20
 Db 106 ATGAATTCATTAATCATCTGAAACACAATGCAAGAGAGAGGATGCTTC---TCTTCC 162
 Qy 21 GluValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle 40
 Db 163 CAAATGTTCTTATGGACTGTGCTGGGATCCCCATCCTATTCTCAGTGCCTGTTTCATC 222
 Qy 41 ThrArgCysValValThrTyArgSerSerGlnIleSerGlyGln---AsnLeuGlnPro 59
 Db 223 ACCAGATGCTGTGTGACATTCGCATCTTTCACACCTGTGATGAGAAAAAGTTTCAGTA 282
 Qy 60 HisArgAenIleLysGluLeuSerCysTySerGluAlaSerGlySerValLysAenCys 79
 Db 283 CCTGAGAAATTCACAGAGCTCTCCTGCTACAAATATGATGATCAGGTTCAGTCAAGAATGT 342
 Qy 80 CysProLeuAenTrpLysHisTyArgSerSerGlnSerSerCysTySerPhePheSerThr 99
 Db 343 TGTCCATTGAACCTGGGAATATTTTCAATCCAGCTGCTACTCTTTCTTACTGACACCAAT 402
 Qy 100 ThrTrpSerSerLeuLysAenCysSerAspMetGlyAlaHisLeuValLysAen 119
 Db 403 TCCTGGCGCTAAGTTTAAAGAACTGCTCAGCCATGCGGGCTCACCCTGGTGGTTATCAAC 462
 Qy 120 ThrGlnGluGlnGluPheLeuPheArgThrLysProLysArgLysGluPheTyrlle 139
 Db 463 TCACAGGAGGAGCAGGAATTCCTTCTTCTACAGAAACCTAAATGAGAGAGAGTATTTTATT 522
 Qy 140 GlyLeuThrAspGlnValValGluGlyGlnTrpGlnTrpValAspAspThrProPheThr 159
 Db 523 GSACTGTGCAGACCAGGTGTGCGAGGGTCACTGGCAATGGGTGGACGCGCACACCTTTGACA 582
 Qy 160 GluSerLeuSerPheTrpAspAlaGlyGluProAsnAenIleValLeuValGluAspCys 179
 Db 583 AAGTCTCTGAGCTTCTGGGATGTAGGGAGACCCCAACACATAGCTACCTCGGAGGACTGT 642
 Qy 180 AlaThrIleArgAspSerSerAenSerArgLysAenTrpAenAspIleProCysPheTyrl 199
 Db 643 GCCACCATGAGAGACTCTTCAAAACCCCAAGGCAAAATTTGGAATGATGTAACCTGTTTCCTC 702
 Qy 200 SerMetProTrpIleCysGluMetProGluIleSerProLeuAsp 214
 Db 703 AATATTATTCGGATTTGTGAATGGTAGGAATAAATCCTTTGAAC 747
 RESULT 6
 ADC78698
 ID ADC78688 standard; cDNA; 997 BP.
 AC ADC78688;
 XX
 DT 01-JAN-2004 (first entry)
 XX Human PRO244 cDNA.
 XX
 KW antiinflammatory; antiulcer; cytostatic; antipsoriatic; antiparkinsonian;
 KW neurotropic; neuroprotective; vasotropic; chemotactic; angiogenic;
 KW neurotrophic; osteopathic; antiasthmatic; antiarthritic; antirheumatic;
 KW antiarteriosclerotic; cardiac; antidiabetic; cerebroprotective;
 KW thrombolytic; immunomodulator; enterocolitis; Zollinger-Ellison syndrome;
 KW gastrointestinal ulceration; psoriasis; cancer; Parkinson's disease;
 KW Alzheimer's; ALS; neuropathy; dermal scarring; wound healing;

KW nerve repair; thrombosis; bone; cartilage formation; angiogenesis;
 KW asthma; rheumatoid arthritis; multiple sclerosis; inflammatory disorder;
 KW atherosclerosis; cardiac injury; infertility; premature aging; AIDS;
 KW diabetes; stroke; gene therapy; transgenic; PRO; human; ss; gene.
 XX Homo sapiens.
 OS
 PN WO200015796-A2.
 XX
 PD 23-MAR-2000.
 XX
 PF 15-SEP-1999; 99WO-US021090.
 XX
 PR 16-SEP-1998; 98WO-US019330.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Chen J, Goddard A, Gurney AL, Hillan K, Pennica D, Wood WI;
 PI Yuan J;
 XX
 DR WPI: 2000-271434/23.
 DR P-PSDB; ADC78689.
 XX
 PT Novel nucleic acids encoding secreted and transmembrane polypeptides with
 PT homology, e.g. to growth and cancer-associated antigens.
 XX
 PS Claim 2; SEQ ID NO 376; 355pp; English.
 XX
 CC The invention relates to a novel nucleic acid encoding a PRO polypeptide.
 CC The polypeptides and polynucleotides of the invention may be useful as
 CC research tools and as therapeutics for treating enterocolitis, Zollinger-
 CC Ellison syndrome, gastrointestinal ulceration, psoriasis, cancer,
 CC Parkinson's disease, Alzheimer's disease, ALS, neuropathies, dermal
 CC scarring and wound healing, nerve repair, thrombosis, bone and/or
 CC cartilage formation, angiogenesis, asthma, rheumatoid arthritis, multiple
 CC sclerosis, inflammatory disorders, atherosclerosis, cardiac injury,
 CC infertility, premature aging, AIDS, diabetes complications and stroke.
 CC The molecules may also be utilised during gene therapy procedures and
 CC transgenic animal production. The current sequence is that of the human
 CC PRO cDNA of the invention.
 XX
 SQ Sequence 997 BP; 376 A; 189 C; 200 G; 232 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 1 41e-72 Length: 997
 Score: 774.00 Matches: 143
 Percent Similarity: 79.07% Conservative: 27
 Best Local Similarity: 66.51% Mismatches: 43
 Query Match: 65.65% Indels: 2
 DB: 3 Gaps: 2
 US-10-812-620-2 (1-214) x ADC78688 (1-997)
 Qy 1 MetAsnSerThrLysSerProAlaSerHisThrLysGlyCysPhenylsAsnSer 20
 Db 106 ATGAATTCATCTAAATCATCTGAAACACAATGCACAGAGAGGATGCTTC---TCTTCC 162
 Qy 21 GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle 40
 Db 163 CAATGTTCTTATGGACTGTGCTGGGATCCCATCTATTCTCAGTGCCTGTTTCATC 222
 Qy 41 ThrArgCysValValThrTrpArgSerSerGlnIleSerGlyGln---AsnLeuGlnPro 59
 Db 223 ACCAGATGTTGTGACATTTGCATCTTTCAAACTGTGATGAGAAAAGTTTCAGCTA 282
 Qy 60 HisArgAsnIleGlyLeuSerCysTyrSerGlnAlaSerGlySerValIysAsnCys 79
 Db 283 CCTGAGAATTTTCACAGAGCTCTCTGCTACAAATATGATGATCAGGTTTCAGTCAAGATTCT 342
 Qy 80 CysProLeuAsnTrpLysHisTyrGlnSerSerCysTyrPhePheSerThrThrLeu 99
 Db 343 TGTCATTGAACGGGAATATTTCATCCAGCTGCTACTTCTTTCTACTGACACCAT 402

Qy 100 ThrTrpSerSerSerLeuLysAsnCysSerAspMetGlyAlaHisLeuValValIleAsp 119
 Db 403 TCCTGGGCGTTAAGTTTAAAGACTGCTCAGCCATGGGGCTCACCTGGTGTATCAAC 462
 Qy 120 ThrGlnGluGluGlnGluPheLeuPheArgThrLysProLysProLysArgLysGluPheTyrIle 139
 Db 463 TCACAGGAGGAGCAGGAATTCCTTCTTACAAAGAAACCTAAATGAGAGAGTTTTTATT 522
 Qy 140 GlyLeuThrAspGlnValValGluGlyGlnTrpGlnTrpValAspAspThrProPheThr 159
 Db 523 GGACTGTGAGACAGGTTGTGAGGTCAGTGGCAATGGTGGAGCGGACACCTTTTGACA 582
 Qy 160 GluSerLeuSerPheTrpAspAlaGlyGluProAsnAsnIleValLeuValGluAspCys 179
 Db 583 AAGTCTCTGAGCTTCTGGGATGTAGGGAGGCCCAACACATAGCTACCTGGAGGACTGT 642
 Qy 180 AlaThrIleArgAspSerSerAsnSerArgLysAsnTrpAsnAspIleProCysPheTyr 199
 Db 643 GCCACCATGAGAGACTCTTCAAAACCCAAAGGCAAAATTCGAATGATGTAACCTGTTTCCTC 702
 Qy 200 SerMetProTrpIleCysGluMetProGluIleSerProLeuAsp 214
 Db 703 AATTATTTTCGATTGTGAAATGTTAGGAATAAATCTTTGAAC 747
 RESULT 7
 AAF72432
 ID AAF72432 standard; cDNA; 997 BP.
 XX
 AC AAF72432;
 XX
 DT 24-APR-2001 (first entry)
 XX
 DE Human PRO244 cDNA.
 XX
 KW Human; PRO; dermatological; antipsoriatic; cytostatic; antiinflammatory;
 KW antiparkinsonian nootropic; neuroprotective; vulnery; cardiant;
 KW antiangiogenic; vasotropic; antiasthmatic; antirheumatic; cancer;
 KW antithratic; antiinfertility; antidiabetic; antiviral; diabetes;
 KW ophthalmological; gene therapy; skin disease; gastrointestinal disorder;
 KW ischaemia; inflammation; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200104311-A1.
 XX
 PD 18-JAN-2001.
 XX
 PF 22-FEB-2000; 2000WO-US004414.
 XX
 PR 07-JUL-1999; 99US-0143048P.
 PR 26-JUL-1999; 99US-0145698P.
 PR 28-JUL-1999; 99US-0146222P.
 PR 08-SEP-1999; 99WO-US020594.
 PR 13-SEP-1999; 99WO-US020944.
 PR 15-SEP-1999; 99WO-US021090.
 PR 15-SEP-1999; 99WO-US021547.
 PR 05-OCT-1999; 99WO-US023089.
 PR 29-NOV-1999; 99WO-US028214.
 PR 30-NOV-1999; 99WO-US028313.
 PR 02-DEC-1999; 99WO-US028564.
 PR 02-DEC-1999; 99WO-US028565.
 PR 16-DEC-1999; 99WO-US030095.
 PR 20-DEC-1999; 99WO-US030911.
 PR 20-DEC-1999; 99WO-US030999.
 PR 05-JAN-2000; 2000WO-US000219.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Botstein D, Deenovers L, Eaton DL, Ferrara N;
 PI Filvaroff E, Fong S, Cao W, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski P, Grimaldi CJ, Gurney AL, Hillan KJ, Kljavin IJ;
 PI Mather JP, Pan J, Paoni NP, Roy MA, Stewart TA, Tumas D;
 PI Williams PW, Wood WI;


```
XX WPI; 2001-081051/09.
DR P-ESDB; AAB80271.
XX
XX Sixty one nucleic acids encoding PRO polypeptides which are useful in the
PT treatment of skin diseases (e.g. psoriasis), cancers (e.g. lung squamous
PT cell carcinoma) and neurodegenerative diseases (e.g. Alzheimer's
PT disease).
XX
XX Claim 2; Fig 121; 393pp; English.
XX
XX The present sequence is one of sixty one nucleic acids encoding novel
CC secreted and transmembrane PRO polypeptides. The PRO polypeptides are
CC useful for treating skin diseases (e.g. psoriasis), cancers (e.g. lung
CC squamous cell carcinoma), gastrointestinal disorders (e.g.
CC enterocolitis), neurodegenerative diseases (e.g. Alzheimer's disease,
CC Parkinson's disease), wound repair, cardiovascular disorders (e.g.
CC endometrial bleeding, angiogenesis, ischaemias such as coronary ischaemia,
CC atherosclerosis), inflammatory disorders (e.g. asthma, rheumatoid
CC arthritis, multiple sclerosis), infertility, AIDS and diabetes and
CC retinal disorders such as retinitis pigmentosum. The PRO nucleic acids
CC have applications in molecular biology, including use as hybridization
CC probes, and in chromosome and gene mapping
XX
SQ Sequence 997 BP; 376 A; 189 C; 200 G; 232 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1-41e-72 Length: 997
Score: 774.00 Matches: 143
Percent Similarity: 79.07% Conservative: 27
Best Local Similarity: 66.51% Mismatches: 43
Query Match: 65.65% Indels: 2
DB: 4 Gaps: 2

US-10-812-620-2 (1-214) x AAF72432 (1-997)

Qy 1 MetAsnSerThrLysSerProAlaSerHisHisThrGluArgGlyCysPheLysAsnSer 20
Db 106 ATGAATTCATCTAAATCATCTGAAACACAAATGCACAGAGAGGATGCTTC---TCITCC 162
Qy 21 GlnValLeuSerThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle 40
Db 163 CAATATGTTCTATGGAGCTGTTGCTGGGATCCCATCTCTATTTCTCAGTGCCTGTTTCATC 222
Qy 41 ThrArgCysValValThrTyArgSerSerGlnIleSerGlyGln---AsnLeuGlnPro 59
Db 223 ACCAGATGTGTGTGACATCTTCGATCTTTCAAACCTGTGTATGAGAAAAGTTTCAGCTA 282
Qy 60 HisArgAsnIleLysGluLeuSerCysTySerGluAlaSerGlySerValLysAsnCys 79
Db 283 CCTGGAATTTTCACAGAGCTCTCTGCTACAAATATGATGATCAGTTCAAGTAATGT 342
Qy 80 CysProLeuAsnTrpLysHisTyGlnSerSerCysTyPhePheSerThrThrLeu 99
Db 343 TGTCCATGAACTGGGAATATTTCAATCCAGCTGCTACTCTCTTTCTACTGACACCAAT 402
Qy 100 ThrTrpSerSerSerLeuLysAsnCysSerAspMetGlyAlaHisLeuValValIleAsp 119
Db 403 TCTCGGGCGTAAAGTTTAAAGAACTGCTCAACCATGGGGCTCACCTGGTGGTTATCAAC 462
Qy 120 ThrGlnGluGlnGlnGluPheLeuPheArgThrLysProLysArgLysGluPheTyrlle 139
Db 463 TCACAGGAGGAGCAGGAATCTCTTCTCAAGAAACCTAAATGACAGAGATTTTATT 522
Qy 140 GlyLeuThrAspGlnValValGluGlyGlnTrpGlnTrpValAspAspThrProPheThr 159
Db 523 GGACTGTGACACCAAGTTGTGAGGGTCAGTGGCAATGGGTGGCGGCACACCTTTGACA 582
Qy 160 GluSerLeuSerPheTrpAspAlaGlyClnProAsnAsnIleValLeuValGluAspCys 179
Db 583 AAGTCTCTGAGCTTCTGGGATGTAGGGAGGCCCAACACATAGCTACCCCTGGAGGACTGT 642
Qy 180 AlaThrIleArgAspSerSerAsnSerArgLysAsnTrpAsnAspIleProCysPheTyrl 199
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Db 643 GCCACCATGAGAGACTCTTCAAAACCCAGGCAAAATGGGAATGATGAACCTGTTCTCTC 702
Qy 200 SerMetProTrpIleCysGluMetProGluIleSerProLeuAsp 214
Db 703 AATTATTTTCGGATTTCGTAATGGTAGGAATAAATCTTTGAAC 747
RESULT 8
AAS45936
ID AAS45936 standard; cDNA; 997 BP.
XX
XX AAS45936;
AC AAS45936;
XX
XX 18-DEC-2001 (first entry)
DT
XX Human DNA encoding PRO polypeptide sequence #12.
DE
XX PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; ss;
KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder;
KW PCR primer.
XX
XX Homo sapiens.
OS
XX WO200168848-A2.
XX
XX 20-SEP-2001.
PD
XX
XX 28-FEB-2001; 2001WO-US006520.
PF
XX
XX 01-MAR-2000; 2000WO-US005601.
PR
XX 02-MAR-2000; 2000WO-US005841.
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XX 03-MAR-2000; 2000US-0187202P.
PR
XX 06-MAR-2000; 2000US-0186988P.
PR
XX 14-MAR-2000; 2000US-0189320P.
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XX 14-MAR-2000; 2000US-0189328P.
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XX 15-MAR-2000; 2000WO-US006884.
PR
XX 21-MAR-2000; 2000US-0190828P.
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XX 21-MAR-2000; 2000US-0191007P.
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XX 21-MAR-2000; 2000US-0191048P.
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XX 21-MAR-2000; 2000US-0191314P.
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XX 28-MAR-2000; 2000US-0192655P.
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XX 29-MAR-2000; 2000US-0193032P.
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XX 29-MAR-2000; 2000US-0193053P.
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XX 30-MAR-2000; 2000US-0193053P.
PR
XX 04-APR-2000; 2000WO-US008439.
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XX 04-APR-2000; 2000US-0194449P.
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XX 11-APR-2000; 2000US-0194647P.
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XX 11-APR-2000; 2000US-0195975P.
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XX 11-APR-2000; 2000US-0196000P.
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XX 11-APR-2000; 2000US-0196187P.
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XX 11-APR-2000; 2000US-0196690P.
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XX 11-APR-2000; 2000US-0196820P.
PR
XX 18-APR-2000; 2000US-0198121P.
PR
XX 18-APR-2000; 2000US-0198585P.
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XX 25-APR-2000; 2000US-0199397P.
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XX 25-APR-2000; 2000US-0199550P.
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XX 25-APR-2000; 2000US-0199654P.
PR
XX 03-MAY-2000; 2000US-0201516P.
PR
XX 17-MAY-2000; 2000WO-US013705.
PR
XX 22-MAY-2000; 2000WO-US014042.
PR
XX 30-MAY-2000; 2000WO-US014941.
PR
XX 02-JUN-2000; 2000WO-US015264.
PR
XX 05-JUN-2000; 2000US-0209832P.
PR
XX 28-JUL-2000; 2000WO-US020710.
PR
XX 22-AUG-2000; 2000US-0064848.
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XX 24-AUG-2000; 2000WO-US023328.
PR
XX 08-NOV-2000; 2000WO-US030952.
PR
XX 01-DEC-2000; 2000WO-US032878.
PR
XX 20-DEC-2000; 2000WO-US034956.
XX
XX (GETH ) GENENTECH INC.
XX
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PI Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
XX
DR WPI: 2001-602746/68.
DR P-PSDB; AAU29035.

XX Novel nucleic acids encoding PRO polypeptides, used to diagnose the
PT presence of tumors, such as prostate and breast tumors, in mammals and to
PT screen for modulators of the compounds.

XX PS Claim 2; Fig 23; 774pp; English.

XX Sequences AAS45925-AAS46231 represent DNA molecules encoding and PCR
CC primers for PRO polypeptides of the invention. The sequences of the
CC invention can be used to detect the presence of a tumour in a mammal by
CC comparing the level of expression of a PRO polypeptide in a test sample
CC of cells from the animal and a control sample of normal cells, whereby a
CC higher level of expression in the test sample indicates the presence of a
CC tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep,
CC pigs, goats and rabbits but are preferably human. The polypeptides can be
CC used to stimulate tumour necrosis factor (TNF) alpha release from human
CC blood, when contacted with it. A specific polypeptide can be used to
CC stimulate the proliferation or differentiation of chondrocyte cells. The
CC PRO proteins can be used to determine the presence of tumours and also
CC susceptibility to tumour development, particularly adrenal, lung, colon,
CC breast, prostate, rectal, cervical, or liver tumours, in mammalian
CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
CC can be used for genetic analysis of individuals with genetic disorders

XX SQ Sequence 997 BP; 376 A; 189 C; 200 G; 232 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1,41e-72 Length: 997
Score: 774.00 Matches: 143
Percent Similarity: 79.07% Conservative: 27
Best Local Similarity: 66.51% Mismatches: 43
Query Match: 65.65% Indels: 2
DB: Gaps: 2

US-10-812-620-2 (1-214) x AAS45936 (1-997)

QY 1 MetAsnSerThrLysSerProAlaSerHisHisThrGluArgGlyCysPheLysAsnSer 20
Db 106 ATGAATTCATCTAAATCATCTCAACACACAAATGCACAGAGAGGATGCTTC---TCTTCC 162
QY 21 GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle 40
Db 163 CAAATGTTCTTATGGACTGTTGCTGGATCCCATCTATTCTCAGTGCCTGTTTCATC 222
QY 41 ThrArgCysValValThrTyrArgSerSerGlnIleSerGlyGln---AsnLeuGlnPro 59
Db 223 ACCAGATGTTGTGACATTTTCGATCTTTCAACCTGTGATGAGAAAAGTTTCAGCTA 282
QY 60 HisArgAsnIleLysGluLeuSerCysTyrSerGluAlaSerGlySerValLysAsnCys 79
Db 283 CTGAGAAATTCACAGAGCTCTCTGCTACAAATATGATGATCAGTTCAAGAAATGT 342
QY 80 CysProLeuAsnTrpLysHisTyrGlnSerSerCysTyrPhePheSerThrThrThrLeu 99
Db 343 TGTCCATTGAATCGGAATATTTTCAATCCAGCTGCTACTTCTTTCTACTGACACCAAT 402
QY 100 ThrTrpSerSerSerLeuLysAsnCysSerAspMetGlyAlaHisLeuValLysLeu 119
Db 403 TCTTGGCGCTTAAGTTTAAGAACTGCTCAGCCATGGGGGCTCAGCTGGTGTATATCAAC 462
QY 120 ThrGlnGluGlnGlnGluPheLeuPheArgThrLysProLysArgLysGluPheTyrIle 139
Db 463 TCACAGGAGGACAGGAATTCCTTCTCCTACAGAAACCTAAATATGAGAGAGTTTATTAT 522
QY 140 GlyLeuThrAspGlnValValGluGlyGlnTrpGlnTrpValAspAspThrProPheThr 159
Db 523 GGACTGTGCAGACAGGTTTCTCGAGGGTCAGTGGCAATGGTGGCGGACACACTTTTGACA 582

QY 160 GluSerLeuSerPheTrpAspAlaGlyGluProAsnAsnIleValLeuValGluAspCys 179
Db 583 AAGTCTCTGAGCTTCTGGATGTAGGGAGCCCAACACATAGCTACCTTGAGGAGCTGT 642
QY 180 AlaThrIleArgAspSerSerAsnSerArgLysAsnTrpAsnAspIleProCysPheTyr 199
Db 643 GCCACCATGAGAGACTCTTCAACCCAGGCAAAATTGAATGATGAACCTGTTTCTCTC 702
QY 200 SerMetProTrpIleCysGluMetProGluIleSerProLeuAsp 214
Db 703 AATTATTTTCGATTGTGAAATGTTAGGAATAAATCTTTTGAAC 747

RESULT 9

ACA60316

ID ACA60316 standard; cDNA; 997 BP.

AC ACA60316;

XX 12-JUN-2003 (first entry)

XX Human cDNA for secreted/transmembrane protein PRO244.

DE Human; ss; gene; secreted protein; transmembrane protein; PRO;
KW gene therapy; chromosome identification; chromosome marker.

XX Homo sapiens.

XX US2003003530-Al.

XX 02-JAN-2003.

XX 11-JUL-2001; 2001US-00904011.

PR 17-SEP-1997; 97US-0059113P.

PR 17-SEP-1997; 97US-0059115P.

PR 17-SEP-1997; 97US-0059117P.

PR 17-SEP-1997; 97US-0059119P.

PR 17-SEP-1997; 97US-0059121P.

PR 17-SEP-1997; 97US-0059124P.

PR 18-SEP-1997; 97US-0059263P.

PR 15-OCT-1997; 97US-0062125P.

PR 17-OCT-1997; 97US-0062285P.

PR 17-OCT-1997; 97US-0062287P.

PR 21-OCT-1997; 97US-0063486P.

PR 24-OCT-1997; 97US-0062814P.

PR 24-OCT-1997; 97US-0062816P.

PR 24-OCT-1997; 97US-0063045P.

PR 24-OCT-1997; 97US-0063120P.

PR 24-OCT-1997; 97US-0063121P.

PR 24-OCT-1997; 97US-0063128P.

PR 27-OCT-1997; 97US-0063327P.

PR 28-OCT-1997; 97US-0063329P.

PR 28-OCT-1997; 97US-0063541P.

PR 28-OCT-1997; 97US-0063542P.

PR 28-OCT-1997; 97US-0063544P.

PR 28-OCT-1997; 97US-0063549P.

PR 28-OCT-1997; 97US-0063550P.

PR 28-OCT-1997; 97US-0063564P.

PR 29-OCT-1997; 97US-0063435P.

PR 29-OCT-1997; 97US-0063704P.

PR 29-OCT-1997; 97US-0063732P.

PR 29-OCT-1997; 97US-0063734P.

PR 29-OCT-1997; 97US-0063738P.

PR 29-OCT-1997; 97US-0063739P.

PR 31-OCT-1997; 97US-0064215P.

PR 31-OCT-1997; 97US-0063870P.

PR 03-NOV-1997; 97US-0064103P.

PR 07-NOV-1997; 97US-0064248P.

PR 12-NOV-1997; 97US-0064809P.

PR 12-NOV-1997; 97US-0065186P.

17-NOV-1997; 97US-0065846P.
 18-NOV-1997; 97US-0065693P.
 21-NOV-1997; 97US-0066120P.
 21-NOV-1997; 97US-0066364P.
 24-NOV-1997; 97US-0066453P.
 24-NOV-1997; 97US-0066466P.
 24-NOV-1997; 97US-0066511P.
 24-NOV-1997; 97US-0066770P.
 24-NOV-1997; 97US-0066772P.
 10-SEP-1998; 98WO-US018824.
 14-SEP-1998; 98WO-US019177.
 16-SEP-1998; 98WO-US019330.
 17-SEP-1998; 98WO-US019437.
 01-DEC-1998; 98WO-US025108.
 08-SEP-1999; 99WO-US020594.
 13-SEP-1999; 99WO-US020944.
 15-SEP-1999; 99WO-US021090.
 15-SEP-1999; 99WO-US021547.
 05-OCT-1999; 99WO-US023089.
 29-NOV-1999; 99WO-US028214.
 30-NOV-1999; 99WO-US028313.
 01-DEC-1999; 99WO-US028301.
 02-DEC-1999; 99WO-US028564.
 02-DEC-1999; 99WO-US028565.
 16-DEC-1999; 99WO-US030095.
 20-DEC-1999; 99WO-US030911.
 20-DEC-1999; 99WO-US030999.
 05-JAN-2000; 2000WO-US000219.
 11-FEB-2000; 2000WO-US003565.
 22-FEB-2000; 2000WO-US004414.
 24-FEB-2000; 2000WO-US005004.
 02-MAR-2000; 2000WO-US005841.
 20-MAR-2000; 2000WO-US007377.
 30-MAR-2000; 2000WO-US008439.
 22-MAY-2000; 2000WO-US014042.
 02-JUN-2000; 2000WO-US015264.
 28-JUL-2000; 2000WO-US020710.
 24-AUG-2000; 2000WO-US023328.
 18-SEP-2000; 2000WO-US0265350.
 (GETH) GENENTECH INC.
 Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
 Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
 Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ;
 Mather JP, Pan J, Paoni NF, Roy WA, Stewart TA, Tumas D;
 Williams PM, Wood WI;
 WPI; 2003-329602/31.
 P-PSDB; ABU71950.
 New transmembrane polypeptides and nucleic acids encoding the
 polypeptides, useful in gene therapy, in chromosome identification, as
 chromosome markers, in generating probes and in tissue typing.
 Claim 2; Fig 121; 484pp; English.
 The invention relates to an isolated nucleic acid with at least 80%
 nucleic acid sequence identity to a nucleotide sequence encoding one of
 61 secreted/transmembrane polypeptides, or PRO polypeptides or encoding a
 PRO protein/extracellular domain. Also included are a vector comprising
 the PRO nucleic acid, a host cell comprising the vector, producing a PRO
 polypeptide (by culturing the host cell for the expression of the PRO
 polypeptide, and recovering the PRO polypeptide from the cell culture),
 an isolated PRO polypeptide (having at least 80% sequence identity to:
 a) an amino acid sequence selected from the 61 PRO proteins; (b) an amino
 acid sequence encoded by a nucleic acid molecule deposited with an ATCC
 number (detailed in the specification); or (c) an extracellular domain of
 a PRO polypeptide or to a PRO polypeptide lacking its associated signal
 peptide), a chimeric molecule comprising a PRO polypeptide of fused to a
 heterologous amino acid sequence, an anti-PRO antibody, detecting a
 PRO245 or PRO1868 in a sample suspected of containing the polypeptide,
 linking a bioactive molecule to a cell expressing a PRO245 or PRO1868 and

modulating at least one biological activity of a cell expressing a PRO245
 or PRO1868. Nucleic acids which encode PRO can be used to generate either
 transgenic animals or knock-out animals which may be used in the
 development and screening of therapeutically useful reagents. The nucleic
 acids may also be used in gene therapy, in chromosome identification, as
 chromosome markers, or in generating probes. The PRO polypeptides are
 useful as molecular markers for protein electrophoresis, and the isolated
 nucleic acids may be used for recombinantly expressing those markers. The
 PRO polypeptides and nucleic acids may also be used in tissue typing.
 Anti-PRO antibodies are useful in diagnostic assays for PRO, and in
 affinity purification of PRO from recombinant cell culture or natural
 sources. The present sequence encodes a PRO protein
 SQ Sequence 997 BP; 376 A; 189 C; 200 G; 232 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 1-41e-72 Length: 997
 Score: 774.00 Matches: 143
 Percent Similarity: 79.07% Conservative: 27
 Best Local Similarity: 66.51% Mismatches: 43
 Query Match: 65.65% Indels: 2
 DB: Gaps: 2
 US-10-812-620-2 (1-214) x ACA60316 (1-997)
 Qy 1 MetAenSerThrLysSerProAlaSerHisHisThrGluArgGlyCysPheLysAenSer 20
 Db 106 ATGAATTCATTAATCATCTGAAACACATGACAGAGAGGATGCTTC--TCTTCC 162
 Qy 21 GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle 40
 Db 163 CAAATGTTCTTATGGACTGTTGCTGGGATCCCCATCTCTATTCTCAGTCGCTTTTCATC 222
 Qy 41 ThrArgCysValValThrTyrArgSerSerGlnIleSerGlyGln--AenLeuGlnPro 59
 Db 223 ACCAGATGTTGTGGACATTTCCGATCTCTTCAACCTGTGTGATGAGAAAAGTTTCAGTA 282
 Qy 60 HisArgAenIleLysGluLeuSerCysTyrSerGluAlaSerGlySerValLysAenCys 79
 Db 283 CCTGAGAAATTCACAGAGCTCTCTCTGCTACAAATATGATGATCAGTTTCAGTCAAGAAATGT 342
 Qy 80 CysProLeuAenTrpLysHisTyrGlnSerSerCysTyrPhePheSerThrThrLeu 99
 Db 343 TGTCCATTGAACCTGGGAATATTTTCAATCCAGCTGTACTTCTTTTCTACTGACACCACT 402
 Qy 100 ThrTrpSerSerSerLysAenCysSerAspMetGlyAlaHisLeuValValIleAsp 119
 Db 403 TCCTGGGCGTTAAGTTTAAAGAACTGCTCAGCCATGGGGGCTCACCTGGTGGTTATCAAC 462
 Qy 120 ThrGlnGluGlnGluPhePheArgThrLysProLysArgLysGluPheTyrIle 139
 Db 463 TCACAGAGGAGCAGGAAATTCCTTCTACAGAAACCTAAATGAGAGAGACTTTTATT 522
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 Qy 160 GluSerLeuSerPheTrpAspAlaGlyGluProAenAenIleValLeuValGluAspCys 179
 Db 583 AAGTCTCTGAGCTCTGGGATGTAGGGGAGGCCCAACAACTAGCTACCTCGGAGGACTGT 642
 Qy 180 AlaThrIleArgAspSerSerAenSerArgLysAenTrpAenAspIleProCysPheTyr 199
 Db 643 GCCACCATGAGAGACTCTTCAACCCCAAGGCAAAATTTGGAATGATGATTAACCTGTTTCTC 702
 Qy 200 SerMetProTrpIleCysGluMetProGluIleSerProLeuAsp 214
 Db 703 AATTATTTCCGATTTCTGAAATGGTAGGAATAAATCCTTTGAAC 747
 RESULT 10
 ACA89386
 ID ACA89386 standard; cdna; 997 BP.
 XX

AC ACA89386;
XX 09-JUL-2003 (first entry)
XX cdNA encoding human PRO polypeptide #12.
XX Human; PRO polypeptide; secreted protein; transmembrane protein;
KW chromosome mapping; gene mapping; tumour; adrenal; lung; colon; breast;
KW prostate; rectal; cervical; liver; cancer; TNF-alpha;
KW tumour necrosis factor-alpha; proliferation; differentiation;
KW chondrocyte cell; bone disorder; cartilage disorder; sports injury;
KW arthritis; cytostatic; antiarthritic; osteopathic; gene therapy; gene;
KW ss.
XX Homo sapiens.
XX OS
XX US2003036141-A1.
XX PD
XX 20-FEB-2003.
XX 01-JUL-2002; 2002US-00187597.
XX 18-SEP-1997; 97US-0059263P.
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PR 25-JUN-1998; 98US-0090690P.
PR 25-JUN-1998; 98US-0090694P.
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PR 26-JUN-1998; 98US-00105413.
PR 26-JUN-1998; 98US-0090862P.
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PR 02-JUL-1998; 98US-0091486P.
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PR 17-AUG-1998; 98US-0096757P.
PR 17-AUG-1998; 98US-0096766P.

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PR 17-AUG-1998; 98US-0096891P.
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PR 18-AUG-1998; 98US-0096959P.
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PR 02-SEP-1998; 98US-0098843P.
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PR 10-SEP-1998; 98US-0099754P.
PR 10-SEP-1998; 98US-0099763P.
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PR 15-SEP-1998; 98US-0100388P.
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PR 18-SEP-1998; 98US-0101014P.
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PR 24-SEP-1998; 98US-0101738P.
PR 24-SEP-1998; 98US-0101739P.
PR 24-SEP-1998; 98US-0101743P.
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PR 25-SEP-1998; 98US-0102207P.
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PR 30-SEP-1998; 98US-0102487P.
PR 30-SEP-1998; 98US-0102570P.
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PR 01-OCT-1998; 98US-0102684P.
PR 01-OCT-1998; 98US-0102687P.

Alignment Scores:
Pred. No.: 1.41e-72
Score: 774.00
Percent Similarity: 79.07%
Best Local Similarity: 66.51%
Query Match: 65.65%
DB: 8

US-10-812-620-2 (1-214) x ACA89386 (1-997)

Qy 1 MetAenSerThrLysSerProAlaSerHisHieThrGluArgGlyCysPheLysAenSer 20
Db 106 ATGAATTCATCTAAATCATCTGAACACAAATGCACAGAGAGGATGCTTC---TCTTCC 162
Qy 21 GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle 40
Db 163 CAAATGTTCTTAUGAGATGTTGCTGGGATCCCATCTATTTCTCACTGCTGCTGTTTCATC 222
Qy 41 ThrArgCysValValThrTyrArgSerSerGlnIleSerGlyGln---AenLeuGlnPro 59
Db 106 ATGAATTCATCTAAATCATCTGAACACAAATGCACAGAGAGGATGCTTC---TCTTCC 162

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Db 223 ACCAGATGTTGTTGACATTTTCGATCTTTCAACCTGTGATGAGAAAAGTTTCAGCTA 282
Qy 60 HisArgAenIleLysGluLeuSerCysTyrSerGluAlaSerGlySerValLysAenCys 79
Db 283 CCTGAGAATTTACAGAGCTCTCTCTGCTACAAATTTATGATCAGGTTTCAGTCAAGAAATTGT 342
Qy 80 CysProLeuAenTrpLysHisTyrGlnSerSerCysTyrPhePheSerThrThrLeu 99
Db 343 TGTCCATTTGAATCGGGAATATTTTCAATCCAGCTGCTACTTCTTTCTACTGACACCATTT 402
Qy 100 ThrTrpSerSerSerLeuLysAenCysSerAspMetGlyAlaHisLeuValValIleAep 119
Db 403 TCTGGCGTTAAGTTTAAAGAACTGCTCAGCCATGGGGGCTCACCTGGTGGTTATCAAC 462
Qy 120 ThrGlnGluGlnGluPheLeuPheArgThrLysProLysArgLysGluPheTyrIle 139
Db 463 TCACAGGAGGAGCAGGAATTTCTTCTTACAGAAACCTTAAATGAGAGAGATTTTTATT 522
Qy 140 GlyLeuThrAspGlnValValGluGlyGlnTrpGlnTrpValAspAspThrProPheThr 159
Db 523 GGAATGTCAGACCAAGGTTGTCAGGGGTTCAGTGGCAATGGGTGGACGGCACACCTTTGACA 582
Qy 160 GluSerLeuSerPheTrpAspAlaGlyGluProAenAenIleValLeuValGluAepCys 179
Db 583 AAGTCTCTGAGCTTCTGGGATGTAGGGGAGCCCAACATAGCTACCTGGAGGACTGT 642
Qy 180 AlaThrIleArgAspSerSerAenSerArgLysAenTrpAenAepIleProCysPheTyr 199
Db 643 GCCACCATGAGAGACTCTTCAACCCCAAGGCAAAATTTGGAATGATGTAACCTGTTTCTTC 702
Qy 200 SerMetProTrpIleCysGluMetProGluIleSerProLeuAep 214
Db 703 AATTATTTTCGGATTTGTAATGTTAGGAATAAATCCTTTTGAAC 747

RESULT 11
ACA73396
ID ACA73396 standard; cDNA; 997 BP.
XX
AC ACA73396;
XX
DT 01-JUL-2003 (first entry)
XX
DE Human secreted/transmembrane protein (PRO) cDNA #12.
XX
KW Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;
KW proliferation; differentiation; chondrocyte cells;
KW tumour necrosis factor-alpha; TNF-alpha; blood; gene therapy.
XX
OS Homo sapiens.
XX
PN US2003036146-A1.
XX
PD 20-FEB-2003.
XX
Qy 02-JUL-2002; 2002US-00187603.
XX
PR 26-JUN-1998; 98US-00105413.
PR 16-SEP-1998; 98WO-US019330.
PR 07-OCT-1998; 98US-00168978.
PR 07-OCT-1998; 98WO-US021141.
PR 06-NOV-1998; 98US-00187368.
PR 01-DEC-1998; 98WO-US025108.
PR 07-DEC-1998; 98US-00202054.
PR 03-MAR-1999; 99US-00254311.
PR 08-MAR-1999; 99WO-US005028.
PR 14-MAY-1999; 99US-00311832.
PR 02-JUN-1999; 99WO-US012252.
PR 25-AUG-1999; 99US-00380137.
PR 25-AUG-1999; 99US-00380138.
PR 25-AUG-1999; 99US-00380139.
PR 25-AUG-1999; 99US-00380142.
PR 01-SEP-1999; 99WO-US020111.

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PR 15-SEP-1999; 99WO-US021090.
 PR 18-OCT-1999; 99US-00403297.
 PR 12-NOV-1999; 99US-00423844.
 PR 01-DEC-1999; 99WO-US028301.
 PR 02-DEC-1999; 99WO-US028551.
 PR 30-DEC-1999; 99WO-US031274.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004413.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 17-MAY-2000; 2000WO-US031709.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 08-JUN-2000; 2000WO-US015264.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 22-AUG-2000; 2000US-00644848.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 18-SEP-2000; 2000US-00664610.
 PR 08-SEP-2000; 2000US-00665350.
 PR 18-NOV-2000; 2000US-00709238.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000US-00747259.
 PR 28-DEC-2000; 2000WO-US034956.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 22-MAR-2001; 2001US-00816744.
 PR 10-MAY-2001; 2001US-00854208.
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 PR 05-JUN-2001; 2001US-00874503.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 18-JUL-2001; 2001US-00908827.
 PR 30-JUL-2001; 2001US-00918585.
 PR 06-AUG-2001; 2001US-00924419.
 PR 13-AUG-2001; 2001US-00929404.
 PR 16-AUG-2001; 2001US-00931836.
 PR 28-AUG-2001; 2001US-00941992.
 PR 29-AUG-2001; 2001WO-US027099.
 PR 04-SEP-2001; 2001US-00946374.
 PR 15-JAN-2002; 2002US-00052586.
 XX (GETH) GENENTECH INC.
 XX
 XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
 PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
 XX P-PSDB; ABU86204.
 DR WPI; 2003-332034/31.
 XX
 XX Three hundred and five nucleic acids encoding PRO polypeptides, useful in
 PT gene therapy, chromosome identification, tissue typing, and for detecting
 PT the presence of tumor in a mammal.
 XX
 XX Claim 2; Fig 23; 707pp; English.
 XX
 XX The invention relates to three hundred and five nucleic acids encoding
 CC PRO polypeptides (secreted and transmembrane), sequences 80% identical to
 CC them, or encoding a PRO polypeptide lacking its associated signal peptide
 CC or an extracellular domain of the PRO polypeptide, with or lacking its
 CC associated signal peptide. Also included are the encoded PRO proteins,
 CC PRO expression vectors, host cells transformed with the vector (used to
 CC produce PRO proteins), a chimeric molecule comprising the PRO
 CC polypeptide fused to a heterologous amino acid sequence, an anti-PRO
 CC antibody, a method for stimulating the release of tumor necrosis factor
 CC alpha (TNF-alpha) from human blood (by contacting the blood with PRO1079,

CC PRO827, PRO791, PRO131, PRO1316, PRO1183, PRO1343, PRO1760, PRO1567 or
 CC PRO4333), a method for stimulating the proliferation or differentiation
 CC of chondrocyte cells by contacting the cells with a PRO6029 polypeptide,
 CC a method for detecting the presence of tumor in a mammal and an
 CC oligonucleotide probe derived from any of the nucleotide sequences cited
 CC above. The PRO polypeptide or anti-PRO antibody is useful for preparing a
 CC medicament for treating a condition that is responsive to the PRO
 CC polypeptide or anti-PRO antibody. The PRO nucleotide sequences are useful
 CC as hybridisation probes in chromosome and gene mapping, or in generating
 CC antisense RNA and DNA. PRO nucleic acids are also useful in preparing PRO
 CC polypeptides, in assays to identify other proteins or molecules involved
 CC in a binding reaction, to generate transgenic animals or knockout
 CC animals, which in turn are useful in the development and screening of
 CC therapeutically useful reagents, for chromosome identification, and
 CC tissue typing. The PRO polypeptides and nucleic acid molecules are also
 CC useful for detecting the presence of a tumour in a mammal, stimulating the
 CC proliferation or differentiation of chondrocyte cells, stimulating the
 CC release of tumour necrosis factor-alpha from human blood, in gene
 CC therapy, or as molecular weight markers for protein electrophoresis
 CC purposes. The anti-PRO antibodies may be used in diagnostic assays for
 CC PRO, or for the affinity purification of PRO from recombinant cell
 CC culture or natural sources. The present sequence is a cDNA encoding a PRO
 CC protein
 XX
 SQ Sequence 997 BP; 376 A; 189 C; 200 G; 232 T; 0 U; 0 Other;

 Alignment Scores:
 Pred. No.: 1.41e-72 Length: 997
 Score: 774.00 Matches: 143
 Percent Similarity: 79.07% Conservative: 27
 Best Local Similarity: 66.51% Mismatches: 43
 Query Match: 65.65% Indels: 2
 DB: 8 Gaps: 2

 US-10-812-620-2 (1-214) x ACA73396 (1-997)

 QY 1 MetAsnSerThrLysSerProAlaSerHisHisThrGluArgGlyCysPheLysAsnSer 20
 DB 106 ATGAATTCATCTTAATCATCTGAAACACAATGCACAGAGAGAGGATGCTTC---TCTTCC 162

 QY 21 GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle 40
 DB 163 CAATGTTCTTATGGACTGTTGCTGGGATCCCATCTTATTTCTCAGTGCCTGTTTCATC 222

 QY 41 ThrArgCysValValThrTyArgSerSerGlnIleSerGlyGln---AsnLeuGlnPro 59
 DB 223 ACCAGATGTTGTGACATTTTCGACATCTTCAAACTCTGTGATGAGAAAAGTTTCAGCTA 282

 QY 60 HisArgAsnIleLysGluLeuSerCysTySerGluAlaSerGlySerValLysAsnCys 79
 DB 283 CTGTGAATTTTCACAGAGCTCTCTGCTACAAATTTATGATGATCAGGTTCAAGAAATGTT 342

 QY 80 CysProLeuAsnTrpLysHisTyArgSerSerCysTySerPhePheSerThrThrLeu 99
 DB 343 TGTCCATTGAACATGGGAATATTTTCAATCCAGCTGCTACTTCTTCTTACTGACACCAT 402

 QY 100 ThrTrpSerSerSerLeuLysAsnCysSerSerMetGlyAlaHisLeuValValIleAsp 119
 DB 403 TCCTGGGGGTTAAGTTTAAAGAACTGCTCAGCCATGGGGGCTCACCCTGGTGGTTATCAAC 462

 QY 120 ThrGlnGluGlnGlnPheLeuPheArgThrLysProLysArgLysGluPheTyIle 139
 DB 463 TCACAGGAGGACAGGAATTCCTTCTCACAAGAAACCTAAATGAGAGAGTTTATTAT 522

 QY 140 GlyLeuThrAspGlnValValGluGlyGlnTrpGlnTrpValAlaAspThrProPheThr 159
 DB 523 GGACTGTCAGACAGGTTGTGAGGGTCAGTGGCAATGGTGGAGCGGCACACCTTTGACA 582

 QY 160 GluSerLeuSerPheTrpAspAlaGlyClnProAsnAsnIleValLeuValGluAspCys 179
 DB 583 AAGTCTCTGAGCTTCTGGGATGTAGGGGAGGCCCAACAACATAGCTTACCTGGAGGACTGT 642

 QY 180 AlaThrIleArgAspSerSerAsnSerArgLysAsnTrpAsnAspIleProCysPheTy 199

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Db      643 GCCACCATGAGAGACTCTTAAACCCAGGCAAAATGGAATGATGTAACCTGTTTCCTC 702
Qy      200 SerMetProTfPilleCysGluMetProGluIleSerProLeuAasp 214
Db      703 AATTATTTCGGAATTTGTAATGCTAGGATAAATCTTTGAAC 747

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ID      ACA05711 standard; cDNA; 997 BP.
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AC      ACA05711;
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XX      29-MAY-2003 (first entry)
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XX      Human secreted/transmembrane protein (PRO) cDNA #12.
XX
XX      Human; Gene; ss: secreted and transmembrane protein; PRO; TNF-alpha;
KW      tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
KW      tissue typing.
XX
XX      Homo sapiens.
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XX      US2003036162-A1.
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PD      20-FEB-2003.
XX
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XX      12-JUL-2002; 2002US-00194423.
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PR      06-NOV-1998; 98US-00187368.
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PR      01-DEC-1998; 98WO-US025108.
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PR      07-DEC-1998; 98US-00202054.
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PR      03-MAR-1999; 99US-00254311.
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PR      08-MAR-1999; 99WO-US005028.
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PR      14-MAY-1999; 99WO-US010733.
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PR      02-JUN-1999; 99WO-US012252.
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PR      01-DEC-1999; 99WO-US028301.
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PR      30-DEC-1999; 99WO-US031274.
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PR      05-JAN-2000; 2000WO-US000219.
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PR      18-FEB-2000; 2000WO-US004341.
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PR      18-FEB-2000; 2000WO-US004342.
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PR      22-FEB-2000; 2000WO-US004414.
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PR      24-FEB-2000; 2000WO-US005004.
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PR      01-MAR-2000; 2000WO-US005601.
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PR      02-MAR-2000; 2000WO-US005841.
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PR      15-MAR-2000; 2000WO-US006884.
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PR      30-MAR-2000; 2000WO-US008439.
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PR      17-MAY-2000; 2000WO-US013705.
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PR      02-JUN-2000; 2000WO-US015264.
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PR      28-JUL-2000; 2000WO-US020710.
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PR      24-AUG-2000; 2000US-00644848.
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PR      22-AUG-2000; 2000WO-US023328.
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PR      18-SEP-2000; 2000US-00654610.
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PR      18-SEP-2000; 2000US-00655350.
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PR      08-NOV-2000; 2000US-00709238.
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PR      08-NOV-2000; 2000WO-US030952.
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PR      01-DEC-2000; 2000WO-US032678.
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PR      20-DEC-2000; 2000US-00747259.
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PR      20-DEC-2000; 2000WO-US034956.
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PR      28-FEB-2001; 2001WO-US006520.
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PR      22-MAR-2001; 2001US-00816744.
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PR      10-MAY-2001; 2001US-00854208.
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PR      10-MAY-2001; 2001US-00854280.
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PR      25-MAY-2001; 2001US-00866028.
PR
PR      01-JUN-2001; 2001WO-US017800.
PR
PR      20-JUN-2001; 2001US-00874503.
PR
PR      29-JUN-2001; 2001WO-US019692.
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PR      09-JUL-2001; 2001WO-US021066.
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PR      18-JUL-2001; 2001US-00908827.
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PR      30-JUL-2001; 2001US-00918585.
PR
PR      06-AUG-2001; 2001US-00924419.
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PR      13-AUG-2001; 2001US-00929404.
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PR      16-AUG-2001; 2001US-00931836.
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PR      28-AUG-2001; 2001US-00941992.
PR
PR      29-AUG-2001; 2001WO-US027099.
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PR      04-SEP-2001; 2001US-00946374.
PR
PR      15-JAN-2002; 2002US-00052586.
XX
XX      (GETH ) GENENTECH INC.
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Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
WPI; 2003-332039/31.
P-PSDB; ABU67417.
```

New secreted and transmembrane PRO polypeptides and nucleic acids, useful in gene therapy, in chromosome and gene mapping, as chromosome markers, in tissue typing, and in chromosome identification.

Claim 2; Fig 23; 706pp; English.

The invention discloses human nucleic acids encoding secreted and transmembrane (PRO) polypeptides. Also disclosed is an antibody that specifically binds to the PRO polypeptide, a method for stimulating the release of tumour necrosis factor alpha (TNF-alpha) from human blood by contacting the blood a PRO polypeptide, a method for stimulating the proliferation or differentiation of chondrocyte cells by contacting the cells with a PRO polypeptide, a method for detecting the presence of a tumour in a mammal and an oligonucleotide probe derived from any of the PRO nucleotide sequences. The nucleotide sequences are useful as probes, in chromosome and gene mapping, in generating antisense RNA and DNA, in preparing PRO polypeptides by recombinant techniques and in gene therapy (e.g. for replacement of defective gene). The PRO polypeptides are useful as molecular weight markers for protein electrophoresis purposes, for chromosome identification, as chromosome markers, as therapeutic agents, for stimulating the release of TNF-alpha from human blood, for stimulating the proliferation or differentiation of chondrocytes and detecting the presence of a tumour. The PRO polypeptides and nucleic acids may also be used diagnostically for tissue typing. The sequences presented in ACA05700-ACA06004 are the cDNAs encoding the PRO polypeptides of the invention

Sequence 997 BP; 376 A; 189 C; 200 G; 232 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.41e-72 Length: 997
Score: 774.00 Matches: 143
Percent Similarity: 79.07% Conservative: 27
Best Local Similarity: 66.51% Mismatches: 43
Query Match: 65.65% Indels: 2
DB: 8 Gaps: 2

US-10-812-620-2 (1-214) x ACA05711 (1-997)

Qy 1 MetAsnSerThrIysSerProAlaSerHisHisThrGluArgGlyCysPheLysAsnSer 20
Db 106 ATGAATTTCATCTAATCATCTGAAACAAATGCACAGAGAGAGATGCTTC---TCTTCC 162

QY 21 GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheile 40
 Db 163 AAAATGTTCTTATGGACTTCTGCGATCCCATCTTATTTCTCAGTCCTGTTTCATC 222
 QY 41 ThrArgCysValValThrTyrArgSerSerGlnIleSerGlyGln---AsnLeuGlnPro 59
 Db 223 ACCAGATGTGTGACATTCGCATCTTCAAACTGTGATGAGAAAAAGTTTCAGCTA 282
 QY 60 HisArgAsnIleGlyGlnLeuSerCysTyrSerGluAlaSerGlySerValIysAsnCys 79
 Db 283 CTGAGAAATTCACAGAGCTCTCCGCTACAAATATGCGATCAGGTTTCAGTCAAGAAATGT 342
 QY 80 CysProLeuAsnTrpLysHisTyrGlnSerSerCysTyrPhePheSerThrThrThrLeu 99
 Db 343 TGTCAATGAATGGGAATATTTTCAATCCAGCTGCTACTTCTTTTCTACTGACCAAT 402
 QY 100 ThrTrpSerSerSerLeuIysAsnCysSerAspMetGlyAlaHisLeuValValIleAsp 119
 Db 403 TCCTGGCGTTAAGTTTAAAGAACTGCTCAGCCATGGGGGCTCACCTGGTGTATCAAC 462
 QY 120 ThrGlnGluGlnGluPheLeuPheArgThrLysProLysArgLysGluPheTyrIle 139
 Db 463 TCACAGGAGGACGAGAAATTCCTTCTCACAAGAAACCTAAATGAGAGAGTTTTTAT 522
 QY 140 GlyLeuThrAspGlnValValGluGlyGlnTrpGlnTrpValAspAspThrProPheThr 159
 Db 523 GGACTGTCTACACAGGTTCTCAGGGTCAGTGGCAATGGTGGACGGCACCTTTTGACA 582
 QY 160 GluSerLeuSerPheTrpAspAlaGlyGluProAsnAsnIleValLeuValGluAspCys 179
 Db 583 AAGTCTCTGAGCTTCTGGGATGTAGGGGAGCCCAACATAGCTACCTCGGAGGACTGT 642
 QY 180 AlaThrIleArgAspSerSerAsnSerArgLysAsnTrpAsnAspIleProCysPheTyr 199
 Db 643 GCCACCATGAGAGACTCTTCAAAACCCAGGCAAAATGGAATCATGTACCTGTTTCTC 702
 QY 200 SerMetProTrpIleCysGluMetProGluIleSerProLeuAsp 214
 Db 703 AATTATTTTCGATTTGTGAAATGGTAGGAATAAAATCTTTTGAAC 747
 RESULT 13
 ID ACA66545 standard; cDNA; 997 BP.
 XX ACA66545;
 AC ACA66545;
 XX
 DT 23-JUN-2003 (first entry)
 XX cDNA encoding human PRO protein #12.
 DE
 XX Human; tumour; adrenal; lung; colon; breast; prostate; rectal; cervical;
 KW liver; PRO; gene therapy; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN US2003036137-A1.
 XX
 PD 20-FEB-2003.
 XX
 PF 27-JUN-2002; 2002US-00184640.
 XX
 PR 26-JUN-1998; 98US-00105413.
 PR 16-SEP-1998; 98WO-US019330.
 PR 07-OCT-1998; 98US-00168978.
 PR 06-OCT-1998; 98WO-US021141.
 PR 06-NOV-1998; 98US-00187368.
 PR 01-DEC-1998; 98WO-US025108.
 PR 07-DEC-1998; 98US-00202054.
 PR 03-MAR-1999; 99US-00254311.
 PR 08-MAR-1999; 99WO-US005028.
 PR 14-MAY-1999; 99US-00311832.
 PR 14-MAY-1999; 99WO-US010733.
 PR 02-JUN-1999; 99WO-US012252.

PR 25-AUG-1999; 99US-00380137.
 PR 25-AUG-1999; 99US-00380138.
 PR 25-AUG-1999; 99US-00380139.
 PR 25-AUG-1999; 99US-00380142.
 PR 01-SEP-1999; 99WO-US020111.
 PR 15-SEP-1999; 99WO-US021090.
 PR 18-OCT-1999; 99US-00403297.
 PR 12-NOV-1999; 99US-00423844.
 PR 01-DEC-1999; 99WO-US028301.
 PR 02-DEC-1999; 99WO-US028551.
 PR 30-DEC-1999; 99WO-US031274.
 PR 05-JAN-2000; 2000WO-US000219.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 24-FEB-2000; 2000WO-US005004.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 02-MAR-2000; 2000WO-US005841.
 PR 15-MAR-2000; 2000WO-US006884.
 PR 30-MAR-2000; 2000WO-US008439.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 22-AUG-2000; 2000US-00644848.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 18-SEP-2000; 2000US-00664610.
 PR 18-SEP-2000; 2000US-00665350.
 PR 08-NOV-2000; 2000US-00709238.
 PR 08-NOV-2000; 2000WO-US010952.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000US-00747259.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 22-MAR-2001; 2001US-00816744.
 PR 10-MAY-2001; 2001US-00854208.
 PR 25-MAY-2001; 2001US-00866028.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 05-JUN-2001; 2001US-00874503.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 09-JUL-2001; 2001WO-US021066.
 PR 18-JUL-2001; 2001US-00908827.
 PR 30-JUL-2001; 2001US-00918585.
 PR 06-AUG-2001; 2001US-00924419.
 PR 13-AUG-2001; 2001US-00929404.
 PR 16-AUG-2001; 2001US-00931836.
 PR 28-AUG-2001; 2001US-00941992.
 PR 29-AUG-2001; 2001WO-US027099.
 PR 04-SEP-2001; 2001US-00946374.
 PR 15-JAN-2002; 2002US-00052586.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
 PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
 XX
 DR WPI; 2003-342038/32.
 DR P-PSDB; ABU80445.
 XX
 PT Three hundred and five nucleic acids encoding secreted and transmembrane
 PRO polypeptides, useful for the diagnosis, prevention and/or treatment
 of tumors, such as adrenal, lung, colon, breast, prostate, rectal,
 cervical or liver tumors.
 XX
 PS Claim 2; Fig 23; 709pp; English.
 XX
 CC The invention relates to three hundred and five nucleic acids encoding
 PRO polypeptides (secreted and transmembrane). Methods and compositions
 of the present invention are useful for the diagnosis, prevention and/or
 treatment of tumours, such as adrenal, lung, colon, breast, prostate, rectal,
 CC

CC rectal, cervical or liver tumours. The PRO polypeptides are also useful
CC as molecular weight markers, or for chromosome identification. The PRO
CC genes are useful as hybridisation probes, or for screening libraries of
CC human cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene
CC therapy, particularly for replacing a defective gene. The present
CC sequence represents a cDNA encoding a human PRO polypeptide of the
CC invention

XX Sequence 997 BP; 376 A; 189 C; 200 G; 232 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.41e-72	Length:	997
Score:	774.00	Matches:	143
Percent Similarity:	79.07%	Conservative:	27
Best Local Similarity:	66.51%	Mismatches:	43
Query Match:	65.65%	Indels:	2
DB:	8	Gaps:	2

US-10-812-620-2 (1-214) x ACA66545 (1-997)

Qy	1	MetAsnSerThrLysSerProAlaSerHisHisThrGluArgGlyCysPheLysAsnSer	20
Db	106	ATGAATTCATCTAAATCATCTGAAACAACATGACAGAGAGGATGCTTC---TCITCC	162
Qy	21	GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle	40
Db	163	CAATATGTTCTTATGGACTCTGCTGGATCCCATCTCTATTTCTCAGTCGCTGTTTCATC	222
Qy	41	ThrArgCysValValThrTyArgSerSerGlnIleSerGlyGln---AsnLeuGlnPro	59
Db	223	ACCAGATGTTGTGGACATTTCCGATCTTCTCAACCTGTGATGAGAAAGATTTCAGCTA	282
Qy	60	HisArgAsnIleLysGluLeuSerCysTy---SerGluAlaSerGlySerValLysAsnCys	79
Db	283	CCTGAGATTTTCACAGAGCTCTCTCTGATCAATTTATGATCAGGTTTCTAGTCACCAATGT	342
Qy	80	CysProLeuAsnTrpLysHisTyGlnSerSerCysTyPhePheSerThrThrLeu	99
Db	343	TGTCATTTGAATCGGAATATTTTCAATCCAGCTGCTACTTCTTTTCTACTGACACCAT	402
Qy	100	ThrTrpSerSerLeuLysAsnCysSerAspMetGlyAlaHisLeuValValIleAsp	119
Db	403	TCCTGGGGCGTTAAGTTTAAAGAACTGCTCAGCCATGGGGGCTCACCTGGTGGTTTATCAAC	462
Qy	120	ThrGlnGluGlnGluPhePheArgThrLysProLysArgLysGluPheTyIle	139
Db	463	TCACAGAGGAGCAGGAATTCCTTCTACAGAAACCTAAATGACAGAGATTTTATT	522
Qy	140	GlyLeuThrAspGlnValValGluGlyGlnTrpGlnTrpValAspAspThrProPheThr	159
Db	523	GGACTGTACAGACCAAGTTGCGAGGGTCAGTGGCAATGGGTGGACGCACACCTTTTGACA	582
Qy	160	GluSerLeuSerPheTrpAspAlaGlyLysProAsnAsnIleValLeuValGluAspCys	179
Db	583	AAGTCTCTGAGCTTCTGGGATGTAGGGAGGCCAACCAACATAGTACCTCTGGAGGACTGT	642
Qy	180	AlaThrIleArgAspSerSerAsnSerArgLysAsnTrpAsnAspIleProCysPheTy	199
Db	643	GCCACCATGAGAGACTCTTCAACCCAGGCAAAATGGAAATGATGTAACCTGTTTCCTC	702
Qy	200	SerMetProTrpIleCysGluMetProGluIleSerProLeuAsp	214
Db	703	AATTATTTCGATTTGTGAAATGGTAGGAATAAATCCTTTGAC	747

RESULT 14

ACD07717

ID ACD07717 standard; DNA; 997 BP.

XX

AC ACD07717;

XX

DT 07-AUG-2003 (first entry)

XX

DE Novel human secreted and transmembrane protein PCR primer #151.

XX	Human; secreted and transmembrane protein; PRO; pharmaceutical;
KW	diagnostic; biosensor; bioindicator; Parkinson's disease;
KW	Alzheimer's disease; inflammation; nephritis; wound healing;
KW	nerve repair; collateral blood vessel formation; cancer;
KW	colorectal cancer; haemorrhage; rheumatoid arthritis; diabetes;
KW	cirrhosis; fibrosis; restenosis; dermal fibrotic condition; keloid;
KW	scarring; ischaemia; stroke; hypertension; heart attack; atherosclerosis;
KW	infertility; gene therapy; PCR; primer; ss.
XX	Homo sapiens.
XX	US2002197671-A1.
PN	26-DEC-2002.
XX	17-JUL-2001; 2001US-00907824.
PR	17-SEP-1997; 97US-0059113P.
PR	17-SEP-1997; 97US-0059115P.
PR	17-SEP-1997; 97US-0059117P.
PR	17-SEP-1997; 97US-0059119P.
PR	17-SEP-1997; 97US-0059121P.
PR	17-SEP-1997; 97US-0059122P.
PR	17-SEP-1997; 97US-0059184P.
PR	18-SEP-1997; 97US-0059263P.
PR	18-SEP-1997; 97US-0059266P.
PR	15-OCT-1997; 97US-0062125P.
PR	17-OCT-1997; 97US-0062285P.
PR	17-OCT-1997; 97US-0062287P.
PR	21-OCT-1997; 97US-0063486P.
PR	24-OCT-1997; 97US-0062814P.
PR	24-OCT-1997; 97US-0062816P.
PR	24-OCT-1997; 97US-0063045P.
PR	24-OCT-1997; 97US-0063120P.
PR	24-OCT-1997; 97US-0063121P.
PR	24-OCT-1997; 97US-0063127P.
PR	24-OCT-1997; 97US-0063128P.
PR	27-OCT-1997; 97US-0063327P.
PR	27-OCT-1997; 97US-0063329P.
PR	28-OCT-1997; 97US-0063341P.
PR	28-OCT-1997; 97US-0063342P.
PR	28-OCT-1997; 97US-0063344P.
PR	28-OCT-1997; 97US-0063349P.
PR	28-OCT-1997; 97US-0063550P.
PR	28-OCT-1997; 97US-0063564P.
PR	29-OCT-1997; 97US-0063435P.
PR	29-OCT-1997; 97US-0063704P.
PR	29-OCT-1997; 97US-0063732P.
PR	29-OCT-1997; 97US-0063734P.
PR	29-OCT-1997; 97US-0063735P.
PR	29-OCT-1997; 97US-0063738P.
PR	29-OCT-1997; 97US-0064215P.
PR	31-OCT-1997; 97US-0063870P.
PR	31-OCT-1997; 97US-0064103P.
PR	03-NOV-1997; 97US-0064248P.
PR	07-NOV-1997; 97US-0064809P.
PR	12-NOV-1997; 97US-0065186P.
PR	17-NOV-1997; 97US-0065846P.
PR	18-NOV-1997; 97US-0065693P.
PR	21-NOV-1997; 97US-0066120P.
PR	21-NOV-1997; 97US-0066364P.
PR	24-NOV-1997; 97US-0066453P.
PR	24-NOV-1997; 97US-0066466P.
PR	24-NOV-1997; 97US-0066511P.
PR	24-NOV-1997; 97US-0066770P.
PR	24-NOV-1997; 97US-0066772P.
PR	10-SEP-1998; 98WO-US018824.
PR	14-SEP-1998; 98WO-US019177.
PR	16-SEP-1998; 98WO-US019330.
PR	17-SEP-1998; 98WO-US019437.
PR	01-DEC-1998; 98WO-US025108.
PR	08-SEP-1999; 99WO-US020594.

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PR 13-SEP-1999; 99WO-US020944.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 05-OCT-1999; 99WO-US023089.
PR 29-NOV-1999; 99WO-US028214.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 05-JAN-2000; 2000WO-US000219.
PR 11-FEB-2000; 2000WO-US003565.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 22-MAY-2000; 2000WO-US014042.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 24-AUG-2000; 2000WO-US023328.
PR 18-SEP-2000; 2000US-00665350.
XX
PA (GETH ) GENENTECH INC.
XX
PI Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Ferrara N;
PI Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;
PI Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, KJavin IJ;
PI Mather JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
PI Williams PM, Wood WT;
XX
XX WPI; 2003-370793/35.
XX
XX New genes and secreted and transmembrane polypeptides (e.g. PRO245 or
PT PRO335), useful for treating or diagnosing e.g. Alzheimer's disease,
PT cancers, hemorrhage, rheumatoid arthritis, diabetes, cirrhosis, ischemia
PT or strokes.
XX
XX Example 51; Page 115; 482pp; English.
XX
XX The invention describes a new isolated nucleic acid molecule comprising
CC the full length coding sequence of the DNA deposited with the American
CC Type Culture Collection (e.g. ATCC Deposit No. 209258), or a sequence
CC with at least 80% identity to a DNA encoding a PRO polypeptide comprising
CC any of 61 sequences having 164-1119 amino acids fully defined in the
CC specification. The PRO polypeptides or polynucleotides are useful as
CC pharmaceuticals, diagnostics, biosensors or bioreactors. These are
CC particularly useful for detecting or treating e.g. Parkinson's disease,
CC Alzheimer's disease, inflammations, nephritis, wound healing, nerve
CC repair, collateral blood vessel formation, cancers (e.g. colorectal
CC cancer), haemorrhage (or reduce risk for haemorrhage), rheumatoid
CC arthritis, diabetes, cirrhosis of the liver, fibrosis of the lungs,
CC restenosis, dermal fibrotic conditions (e.g. keloids or scarring),
CC ischaemia, strokes, hypertension, heart attacks, atherosclerosis, or
CC infertility in mammals (e.g. humans, dogs, cats, cattle, horses, sheep,
CC pigs, goats, or rabbits) The PRO polypeptides are useful as targets for
CC therapeutic intervention in these diseases, and diagnostic determination
CC of the presence of these diseases. The PRO polypeptides are also useful
CC as molecular weight markers, or for chromosome identification. The PRO
CC genes are useful as hybridisation probes, or for screening libraries of
CC human cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene
CC therapy, particularly for replacing a defective gene. This sequence
CC represents a novel human secreted and transmembrane PRO polypeptide
CC associated primer
XX
XX Sequence 997 BP; 376 A; 189 C; 200 G; 232 T; 0 U; 0 Other;
SQ
Alignment Scores:
Pred. No.: 1,41e-72 Length: 997
Score: 774.00 Matches: 143
Percent Similarity: 79.07% Conservative: 27
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Best Local Similarity: 66.51% Mismatches: 43
Query Match: 65.65% Indels: 2
DB: 8 Gaps: 2
US-10-812-620-2 (1-214) x ACD07717 (1-997)
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QY 21 GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle 40
163 CAAATGTTCTTATGGACTGTGTCTGGGATCCCATCTCTATTCTCAGTCGCTGTTTCATC 222
QY 41 ThrArgCysValValThrTyrArgSerSerGlnIleSerGlyGln---AsnLeuGlnPro 59
223 ACCAGATGTGTGTGCATATTTCGCATCTTTCAAACCTGTGATGAGAAAAGTTTCAGCTA 282
QY 60 HisArgAenIleLysGluLeuSerCysTyrSerGluAlaSerGlySerValLysAenCys 79
283 CCTGAGAAATTCACAGAGCTCTCTCTGTACAAATATTGATGATCAGTTCAGTCAAGAATTGT 342
QY 80 CysProLeuAenTrpLysHisTyrGlnSerSerCysTyrPhePheSerThrThrLeu 99
343 TGTCCATTGAACCTGGGAATATTTCATCCAGCTGCTACTCTCTTTCTACTGACACCAATT 402
QY 100 ThrTrpSerSerSerLeuLysAenCysSerSerMetGlyAlaHisLeuValIleAep 119
403 TCCTGGGGCGTTAAGTTTAAAGAACTGCTCAGCCATGGGGGCTCACCCTGGTGGTTATCAAC 462
QY 120 ThrGlnGluGluGlnGluPheLeuPheArgThrLysProLysArgLysGluPheTyrIle 139
463 TCACAGAGAGGACGAGAAATTCCTTCTACAGAAACCTAAATACGAGAGAGTTTTTATT 522
QY 140 GlyLeuThrAepGlnValValGluGlyGlnTrpGlnTrpValAepAepThrProPheThr 159
523 GGACTGTGCAGACCAAGGTTGTGAGGGTCAGTGGCAATGGGTGGACGGACACCTTTTGACA 582
QY 160 GluSerLeuSerPheTrpAepAlaGlyGluProAenAenIleValLeuValGluAepCys 179
583 AAGTCTCTGAGCTCTCTGGGATGTAGGGAGGCCCAACAACATAGCTACCTGTGAGGAGCTGT 642
QY 180 AlaThrIleArgAepSerSerAenSerArgLysAenTrpAenAepIleProCysPheTyr 199
643 GCCACCATGAGAGACTCTTCAAACCCAGCAAAATTCGAATGATGATGAACCTGTTTCTCTC 702
QY 200 SerMetProTrpIleCysGluMetProGluLeuSerProLeuAep 214
703 AATTATTTTCGGATTGTGAAATGTTAGGAATAAATCTCTTTGAAC 747
RESULT 15
ACF20120
ID ACF20120 standard; cDNA; 997 BP.
XX
XX ACF20120;
XX
XX DT 18-SEP-2003 (first entry)
XX
XX Human secreted polypeptide PRO244-encoding cDNA, SEQ ID NO:23.
XX
XX KW Human; PRO; secreted protein; transmembrane protein;
XX extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
XX chondrocyte; proliferation; differentiation; cartilage disorder;
XX bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
XX adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
XX liver; drug screening; transgenic animal; genetic analysis;
XX antiarthritic; vulnery; gene therapy; gene; ss.
XX
XX OS Homo sapiens.
XX
XX PN US2003040063-A1.
XX
XX PD 27-FEB-2003.
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PR 10-SEP-1998; 98US-0099754P.
PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099812P.
PR 15-SEP-1998; 98US-0100388P.
PR 16-SEP-1998; 98US-0100662P.
PR 16-SEP-1998; 98US-0100664P.
PR 16-SEP-1998; 98US-0101751P.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98US-0100683P.
PR 17-SEP-1998; 98US-0100684P.
PR 17-SEP-1998; 98US-0100919P.
PR 17-SEP-1998; 98US-0100930P.
PR 18-SEP-1998; 98US-0100849P.
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PR 23-SEP-1998; 98US-0101471P.
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PR 01-OCT-1998; 98US-0102684P.
PR 01-OCT-1998; 98US-0102687P.
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Alignment Scores:

Pred. No.: 1,41e-72 Length: 997
Score: 774.00 Matches: 143
Percent Similarity: 79.07% Conservative: 27
Best Local Similarity: 66.51% Mismatches: 43
Query Match: 65.65% Indels: 2
DB: 8 Gaps: 2

US-10-812-620-2 (1-214) x ACF20120 (1-997)

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QY 1 MetAsnSerThrLysSerProAlaSerHisHisThrGluArgGlyCysPheLysAsnSer 20
DB 106 ATGAATTTCATTAATCTCTGAAACAAATGCACAGAGAGAGATGCTTC---TCTTCC 162
QY 21 GlnValLeuSerTriphThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle 40
DB 163 CAAATGTTCTTATGGACTGTGCTGGGATCCCCATCCCTATTTCTCAGTGCCTGTTTCATC 222
QY 41 ThrArgCysValValThrTyrArgSerSerGlnIleSerGlyGln---AsnLeuGlnPro 59
DB 223 ACCAGATGTGTGTGCATTTGCGCATCTTTCAAACCTGTGTGATGAGAAAAAGTTTCAGCTA 282
QY 60 HisArgAsnIleLysGluLeuSerCysTyrSerGluAlaSerGlySerValLysAsnCys 79
DB 283 CCTGAGAATTTTCACAGAGCTCTCCTGCTACAATATGGAATTCAGTTCAGTCAAGAATTGT 342
QY 80 CysProLeuAsnTriLysHisTyrGlnSerSerCysTyrPhePheSerThrThrThrLeu 99
DB 343 TGTCATTTGAATGGGAATATTTTCAATCCAGCTGCTACTTCTTTTCTACTGACACCATT 402
QY 100 ThrTriPserSerSerLeuLysAsnCysSerAspMetGlyAlaHisLeuValValIleAsp 119
DB 403 TCCTGGCGCTTAAGTTTAAAGAACTGCTCAGCCATGGGGGCTCACCTGGTGGTATTCAAC 462
QY 120 ThrGlnGluGluGlnGluPheArgThrLysProLysArgLysGluPheTyrIle 139
DB 463 TCACAGGAGGAGCAGGAATTCCTTCTCCTACAGAAACCTTAAATCAGAGAGATTTTATT 522
QY 140 GlyLeuThrAspGlnValValGluGlyGlnTrpGlnTrpValAspAspThrPropheThr 159
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DB 523 GGACTGTTCAGACCAGGTTGTCAGGGTTCAGTGGCAATGGGTGGACGGCACACCTTTTGACA 582
QY 160 GluSerLeuSerPheTriPAspAlaGlyGluProAsnAsnIleValLeuValGluAspCys 179
DB 583 AAGTCTCTGAGCTTCTTGGGATGTAGGGAGGCCCAACAACATAGCTTACCTGGAGGACTGT 642
QY 180 AlaThrIleArgAspSerSerAsnSerArgLysAsnTriPAsnAspIleProCysPheTyr 199
DB 643 GCCACCATGAGAGACTCTTCAAAACCAAGGCANAATTGGAATGATGTAACCTGTTTCCTC 702
QY 200 SerMetProTriPileCysGluMetProGluIleSerProLeuAsp 214
DB 703 AATTATTTTCGATTTGTGAAATGTTAGGAATAAATCCTTTGAAC 747
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Search completed: June 9, 2005, 14:18:24
Job time : 547 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: June 9, 2005, 12:24:29 ; Search time 3168 Seconds
(without alignments)
2571.261 Million cell updates/sec

Title: US-10-812-620-2

Perfect score: 1179

Sequence: 1 MNSTKSPASHHTGCGFKNS.....IPCFYMPWICEMPEISPLD 214

Scoring table:

BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgn2_1/USPTO_spool/US10812620/runat_07062005_124337_3256/app_query_faeta_1.391
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-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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Database :

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8: gb_g881.*
9: gb_g882.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1002.5	85.0	660	2 B2292395	601057892
3	961.5	81.6	717	6 BY743963	BY743963
4	949	80.5	644	4 BG080418	H3053D08-
5	944.5	80.1	667	6 BY747840	BY747840
6	944	80.1	4017	3 AK036493	Mus muscu
7	942	79.9	674	6 BY744630	BY744630
8	936	79.4	655	6 BY749084	BY749084
9	928	78.7	666	6 BY747821	BY747821

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11	917	77.8	645	6	BY743467	BY743467	
12	905	76.8	643	6	BY743813	BY743813	
13	808	68.5	671	6	BY749488	BY749488	
14	735.5	62.4	1032	2	BE311916	601143328	
15	730	61.9	486	5	BY516799	BY516799	
16	725	61.5	588	7	CV025793	3570 Full	
C	17	687.5	58.3	751	7	CN480864	UI-H-Ft2-
C	18	685	58.1	889	4	CG164873	602343809
C	19	660.5	56.0	722	6	CD364806	UI-H-Ft2-
C	20	649.5	55.0	718	6	CB528932	UI-H-Ft2-
C	21	637	54.0	614	6	CB474859	ins09_D09
C	22	631	53.5	618	6	CB453374	708350 MA
C	23	625.5	53.1	738	5	BQ004812	UI-H-E10-
C	24	623	52.8	691	6	CD742945	UI-H-Ft1-
C	25	608	51.6	473	2	BB860060	BB860060
C	26	606	51.4	645	6	CD368203	UI-H-Ft1-
C	27	602	51.1	404	5	BY201224	BY201224
C	28	602	51.1	405	5	BY161340	BY161340
C	29	584	49.5	402	5	BY161525	BY161525
C	30	579	49.1	401	2	AW908017	ur95f12.y
C	31	564	47.8	358	5	BY200082	BY200082
C	32	564	47.8	383	5	BY172432	BY172432
C	33	556	47.2	414	5	BY207927	BY207927
C	34	539	45.7	375	5	BY171319	BY171319
C	35	525	44.5	368	5	BY177981	BY177981
C	36	516	43.8	372	5	BY179745	BY179745
C	37	513	43.5	361	5	BY203558	BY203558
C	38	512	43.4	577	6	CD369372	UI-H-Ft1-
C	39	511.5	43.4	1221	4	BM561994	AGENCOURT
C	40	510	43.3	415	2	BB850328	BB850328
C	41	505	42.8	398	5	BY160494	BY160494
C	42	493	41.8	352	5	BY184536	BY184536
C	43	491	41.6	387	5	BY155120	BY155120
C	44	489	41.5	393	5	BY161254	BY161254
C	45	489	41.5	393	5	BY167126	BY167126

ALIGNMENTS

RESULT 1

AK089286

LOCUS

DEFINITION

AK089286 2233 bp mRNA linear HTC 03-APR-2004
Mus musculus B6-derived CD11 +ve dendritic cells cDNA, RIKEN
full-length enriched library, clone:F730001C01 product:c-type
(calcium dependent, carbohydrate recognition domain) lectin,
superfamily member 9, full insert sequence.

AK089286

VERSION AK089286.1 GI:26105181

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

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TITLE

JOURNAL

MEDLINE

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AUTHORS

Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsunura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
11076861

TITLE
JOURNAL
REFERENCE
AUTHORS

The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)

TITLE
JOURNAL
REFERENCE
AUTHORS

The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 2233)

TITLE
JOURNAL
REFERENCE
AUTHORS

Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
Direct Submission

TITLE
JOURNAL

Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsr.riken.jp, URL:http://genome.gsc.riken.jp/, tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.
Please visit our web site for further details.
URL:http://genome.gsc.riken.jp/
URL:http://fantom.gsc.riken.jp/
Location/Qualifiers

FEATURES

Source

1. .2233
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM DB:F730001C01"
/db_xref="taxon:10090"
/clone="F730001C01"
/cell_type="B6-derived CD11 +ve dendritic cells"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
1. .2233

misc_feature

/note="C-type (calcium dependent, carbohydrate recognition domain) lectin, superfamily member 9 (MGD|MG1:1861232, GB|NM_019948, evidence: BLASTN, 99%, match=1386)"

ORIGIN

Alignment Scores:
Pred. No.: 3,36e-111 Length: 2233
Score: 1116.00 Matches: 211
Percent Similarity: 88.66% Conservative: 0
Best Local Similarity: 88.66% Mismatches: 3

Query Match: 94.66% Indels: 25
DB: 3 Gaps: 1
US-10-812-620-2 (1-214) x AK089286 (1-2233)
QY 1 MetAnSerThrLysSerProAlaSerHisHisThrGluArgGlyCysPheLysAsnSer 20
|||||
Db 124 ATGAATTCAACCAATCGCTGCATCCACACACAGAGAGAGGATGCTTCAAAATCC 183
QY 21 GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle 40
|||||
Db 184 CAAAGTGTCTCTCTGACGATAGCCGGGCTCCATCTCTGTTCTCAGTGGCTGTTTCATC 243
QY 41 ThrArgCysValValThrTyrArgSerSerGlnIleSerGlyGlnAsnLeuGlnProHis 60
|||||
Db 244 ACCAGTGTGTCTGAACATATCGCTGCTCTCAATTTCCGGCAGAACTTACAGGCACAT 303
QY 61 ArgAsnIleLysGluLeuSerCysTyrSerGluAlaSer----- 73
|||||
Db 304 AGAATATTAAGGAGCTTTCTCTGTACAGTGAGGCATCAGGTATAACCATCTGCAGCACA 363
QY 74 -----GlySerVal 76
Db 364 CAGAATCATTTAGCAAAAGTTTCTGGGCAATGTCTGAAGCCTTTCTCTCTTAGGTTTCAGTC 423
QY 77 LysAsnCysCysProLeuAsnTrpLysHisTyrGlnSerSerCysTyrPhePheSerThr 96
|||||
Db 424 AAGAATTGCTGTCTTGAATCGGAACATTAATCAATCTAGTTGTATATTTTTTCTCTAGC 483
QY 97 ThrThrLeuThrTrpSerSerSerLeuLysAsnCysSerAspMetGlyAlaHisLeuVal 116
|||||
Db 484 ACAACCTTGACCTGTGTCATCAAG-TTAAAGAAATGCTCAGACATGGGGCTCACCTGGTG 542
QY 117 ValIleAspThrGlnGluGlnGluPheLeuPheArgThrLysProLysArgLysGlu 136
Db 543 GTTATCGACACACAGAGAAAGAGCAGGAATTCCTTTTTCGCACAAAACCTTAAAAAGGAAGAG 602
QY 137 PheTyrIleGlyLeuThrAspGlnValValGluGlyGlnTrpGlnTrpValAspAspThr 156
Db 603 TTTTATATTGGACTGACAGACCAGGTGGTGGAGGTGAGTGGCAATGGGTGGATATATACA 662
QY 157 PropheThrGluSerLeuSerPheTrpAspAlaGlyGluProAsnAsnIleValLeuVal 176
Db 663 CTTTTCACAGAGTCTCTGAGCTTCGGGATGCTGGGAGCCCAACAATATAGTATTTGGTG 722
QY 177 GluAspCysAlaThrIleArgAspSerSerAsnSerArgLysAsnTrpAsnAspIlePro 196
Db 723 GAGGACTGTGCCACCATTAAGGAGACTCTTCAAACTCCAGGAAGATCTGGAAATGATATACCC 782
QY 197 CysPheTyrSerMetProTrpIleCysGluMetProGluIleSerProLeuAsp 214
Db 783 TGTTTCTACAGTATGCTTGGATTGTGAGATGCCAGAAATTAAGTCTCTCGAC 836

RESULT 2
LOCUS BE292395
DEFINITION 601057892F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:3158063 5', mRNA sequence.
ACCESSION BE292395
VERSION BE292395
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 660)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-romail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.

sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Tissues were provided by David A. Hume (Depts. of Biochemistry and Microbiology/Parasitology Institute for Molecular Bioscience University of Queensland Brisbane, Q 4072 Australia) whose assistance we gratefully acknowledge.

Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

FEATURES

source Location/Qualifiers

1. 717

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="I830025C13"

/tissue_type="bone marrow"

/cell_type="macrophage"

/clone_lib="RIKEN full-length enriched, bone marrow macrophage"

ORIGIN

Alignment Scores:

Pred. No.: 6.17e-95 Length: 717

Score: 961.50 Matches: 187

Percent Similarity: 95.94% Conservative: 2

Best Local Similarity: 94.92% Mismatches: 7

Query Match: 81.55% Indels: 3

DB: 6 Gaps: 1

US-10-812-620-2 (1-214) x BY743963 (1-717)

QY 1 MetAenSerThrylsSerProAlaSerHisHieThrGluArgGlyCysPhelylsenSer 20

DB 123 ATGAATTTCACCAAAATCGCTGCATCCACCACAGAGAGAGGATGCTTCAAAAACCTCC 182

QY 21 GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle 40

DB 183 CAAGTGCTCTCTGGACGATAGCCGGGGCTCCATCTGTTTCTAGTGGCTGTTTCATC 242

QY 41 ThrArgCysValValThrTyrArgSerSerGlnIleSerGlyGlnAsnLeuGlnProHis 60

DB 243 ACCAGATGTGCTGAACATATCGACGCTCTCAAAATTCGGGCGAGAACTTACAGCCACAT 302

QY 61 ArgAsnIlelysGluLeuSerCysTyrSerGluAlaSerGlySerVallylsenCysCys 80

DB 303 AGAAATATTAAAGAGCTTCTCGTACAGTGAGGCATCAGGTTTCAGTCAAGAAATGCTGT 362

QY 81 ProLeuAsnTrpLysHisTyrGlnSerSerCysTyrPhePheSerThrThrThrLeuThr 100

DB 363 CTTTGAACCTGGAACATATATCAATCTAGTGTATTATTTTCTACGACAACTTGACC 422

QY 101 TrpSerSerSerLeuLysAsnCysSerAspMetGlyAlaHisLeuValValIleAspThr 120

DB 423 TGGTCATCAAGTTTAAAGAAATGCTCAGACATGGGGGCTCACCTGGTGTATCGACACA 482

QY 121 GlnGluGlnGlnGluPheLeuPheArgThrLysProLysArglysGluPheThrIleGly 140

DB 483 CAGGAGAGACAGGAATTCCTTTTTCGCACANAACCTTANAAGGAAGAGTTTATATTGGA 542

QY 141 LeuThrAspGlnValValGluGlyGlnTrpGlnTrpValAspAspThrProPheThrGlu 160

DB 543 CTGACAGACAGGTGGTGGAGGGTCAGTGGCAATGGTGGATGATACACCTTTCACAGAG 602

QY 161 SerLeuSerPheTrpAspAlaGlyGluProAsnAsnIleValLeuValGluAspCysAla 180

DB 603 TCCCTGAGCTTCTGGGATGCTGGGAGGCCAACAT-ATAGTTTTCGGAGGACTGTGC- 660

QY 181 ThrIleArgAspSerSerAsnSerArgLyAsnTrpAsnAspIleProCys 197

DB 661 ACCATAGGAGCTCTTCAACTCCACAGAA---CTGGATGATATACCTGT 708

RESULT 4

LOCUS BG080418

DEFINITION BG080418 5' mRNA linear EST 17-DEC-2003

ACCESSION BG080418

VERSION BG080418.2 GI:40014148

KEYWORDS EST.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 644)

AUTHORS Tanaka, T.S., Jaradat, S.A., Lim, M.K., Kargul, G.J., Wang, X., Grahovac, M.J., Pantano, S., Sano, Y., Piao, Y., Nagaraja, R., Dol, H., Wood, W.H. III, Becker, K.G. and Ko, M.S.H.

TITLE Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (16), 9127-9132 (2000)

MEDLINE 20381348

PUBMED 10922068

COMMENT On Jan 26, 2001 this sequence version replaced gi:12562986.

Other ESTs: H3053D08-3

Contact: George J. Kargul

Laboratory of Genetics

National Institute on Aging/National Institutes of Health

333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA

Email: cdna@gsun.grc.nia.nih.gov

This clone set has been freely distributed to the community. Please visit <http://1gsun.grc.nia.nih.gov/cDNA/15k.html> for details.

Plate: H3053 row: D column: 08

Seq primer: -21M13 Reverse

High quality sequence stop: 644

POLYA=No.

Location/Qualifiers

1. 644

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6J"

/db_xref="niaEST:H3053D08-5"

/db_xref="taxon:10090"

/clone="H3053D08"

/sex="Clones arrayed from a variety of cDNA libraries"

/dev_stage="Clones arrayed from a variety of cDNA libraries"

/lab_host="DH10B"

/clone_lib="NIA Mouse 15K cDNA Clone Set"

/note="Vector: pSPORT1; Site 1: SalI; Site 2: NotI; This clone is among a rearranged set of 15,247 clones from 11 embryo cDNA libraries (including preimplantation stage embryos from unfertilized egg to blastocyst, embryonic part of E7.5 embryos, extraembryonic part of E7.5 embryos, and E12.5 female mesonephros/gonad) and one newborn ovary cDNA library. Average insert size 1.5 kb. All source libraries are cloned unidirectionally with Oligo(dT)-Not primers. References include: (1) Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray, 2000, Proc. Natl. Acad. Sci. U.S.A. 97: 9127-9132; (2) Large-scale cDNA analysis reveals phased gene expression patterns during preimplantation mouse development, 2000, Development, 127: 1737-1749; (3) Genome-wide mapping of unselected transcripts from extraembryonic tissue of 7.5-day mouse embryos reveals enrichment in the t-complex and under-representation on the X chromosome, 1998, Hum Mol Genet 7: 1967-1978."

ORIGIN

Alignment Scores:

Pred. No.: 1.25e-93 Length: 644
Score: 949.00 Matches: 178
Percent Similarity: 99.44% Conservative: 0
Best Local Similarity: 99.44% Mismatches: 1
Query Match: 80.49% Indels: 1
DB: 4 Gaps: 0

US-10-812-620-2 (1-214) x BG080418 (1-644)

QY 1 MetAenSerThrLysSerProAlaSerHisThrGluArgGlyCysPheLysAenSer 20
DB 109 ATGAATTCACCAATCGCTCCATCCACACAGAGAGAGATGCTTCACAAACTCC 168
QY 21 GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle 40
DB 169 CAAGTGCTCTCTGGAGCATAGCCGGGGCTCCATCTGTTCTCAGTGGCTGTTTATC 228
QY 41 ThrArgCysValValThrTyrArgSerSerGlnIleSerGlyGlnAenLeuGlnProHis 60
DB 229 ACCAGATGTGTGTAACATATCGAGCTCTCAAAATTTCCGGGACAGAACTTACAGCCACAT 288
QY 61 ArgAenIleLysGluLeuSerCysTyrSerGluAlaSerGlySerValLysAenCysCys 80
DB 289 AGAAATATTAAAGGAGCTTCTCTGTACAGTACGAGCATCAGGTTTCAGTCAAGAAATGCTGT 348
QY 81 ProLeuAenTrpLysHisTyrGlnSerSerCysTyrPhePheSerThrThrLeuThr 100
DB 349 CCTTTGAACTGGAAACATATCAATCTAGTTGTTATTTTCTCTACGACAACTTGACC 408
QY 101 TrpSerSerLeuLysAenCysSerAspMetGlyAlaHisLeuValLysIleAspThr 120
DB 409 TGGTCATCAAGTTTAAAGAAATTTCTCAGACATGGGGCTCACCTGGTGTATTCGACACA 468
QY 121 GlnGluGlnGlnPheLeuPheArgThrLysProLysArgLysGluPheTyrIleGly 140
DB 469 CAGGAAGACGAGGAATTCCTTTTCGACAAACCTTAAAGGAAGAGATTTTATATTGGA 528
QY 141 LeuThrAspGlnValValGluGlyGlnTrpGlnTrpValAspAspThrProPheThrGlu 160
DB 529 CTGACACACACAGTGTGTGGAGGTTCAGTGGCAATGGGTGGATGATACACCTTTCACAGAG 588
QY 161 SerLeuSerPheTrpAspAlaGlyGluProAenAenIleValLeuValGluAspCys 179
DB 589 TCCCTGAGCTTCTGGGATGCTGGGAGGCCAC-AATATAGTTTTTGGTGGAGGACTGT 644

RESULT 5

BY747840 667 bp mRNA linear EST 17-DEC-2002
LOCUS BY747840.1 GI:27176343
DEFINITION dendritic cells Mus musculus cDNA clone F630012G18 5', mRNA
sequence.

ACCESSION

BY747840

BY747840.1 GI:27176343

EST.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 667)

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,

Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,

Schonbach, C., Gojbori, T., Baldarelli, R., Hill, D. P., Buit, C.,

Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H.,

Batalov, S., Beisel, K. W., Blake, J. A., Bradt, D., Brusci, V.,

Chothia, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A.,

Fletcher, C. P., Forrest, A., Frazer, K. S., Gaasterland, T.,

Gariboldi, M., Giasi, C., Godzik, A., Gough, J., Grimmond, S.,

Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A.,

Kawaj, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Konagaya, A.,

Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R.,

Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,
Numata, K., Okido, T., Pavan, W. J., Perte, G., Pesole, G.,
Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S.,
Ravasi, T., Reed, J. C., Reed, D. J., Reid, J., Ring, B. Z., Ringwald, M.,
Sandelin, A., Schneider, C., Semple, C. A., Setou, M., Shimada, K.,
Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M.,
Verardo, R., Wagner, L., Wahlstedt, C., Wang, Y., Watanabe, Y.,
Wells, C., Wilming, L. G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,
Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,
Hayate, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,
Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,
Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,
Shingawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S.,
Rogers, J., Birney, E. and Hayashizaki, Y.

TITLE

Analysis of the mouse transcriptome based on functional annotation

of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

22354683

PUBMED

COMMENT

Contact: Yoshihide Hayashizaki

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Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-res@gsr.riken.jp, URL: http://genome.gsc.riken.jp/

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P.,

Fukuda, S., Hashizume, W., Hayashida, K., Hirozane, T., Hori, F.,

Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y.,

Kondo, S., Konno, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M.,

Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Saito, T., Sakazume, N.,

Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M.,

Takeda, Y., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y.

Direct Submission

Computational Analysis of Full-Length Mouse cDNAs Compared with

Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

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prepare full-length cDNA libraries for rapid discovery of new

genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format

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10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA

encyclopedia: real-time sequence clustering for construction of a

nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

cDNA library was prepared and sequenced in Mouse Genome

Encyclopedia Project of Genome Exploration Research Group in Riken

Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to

prepare mouse tissues

Tissues were provided by Dr. John Todd (Dept. of Medical Genetics

Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome

Trust/MRC building Addenbrookes Hospital Cambridge) whose

assistance we gratefully acknowledge.

Please visit our web site (http://genome.gsc.riken.go.jp) for

further details.

Location/Qualifiers

1. 667

/organism="Mus musculus"

/mol_type="mRNA"

/strain="NOD"

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/clone_id="F630012G18"

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+ve dendritic cells"

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Best Local Similarity: 94.39%	Mismatches: 7	
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DB: 6	Gaps: 1	
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Qy	21 GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle	40
Db	135 CAAGTGCTCTCTGGACGATACCGGGGCTCCATCTGTTCTCAGTGGCTGTTTCATC	194
Qy	41 ThrArgCysValValThrTyrArgSerSerGlnIleSerGlyGlnAenLeuGlnProHis	60
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Qy	61 ArgAenIleLysGluLeuSerCysTyrSerGluAlaSerGlySerValLysAenCysCys	80
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Qy	81 ProLeuAenTrpLysHisTyrGlnSerSerCysTyrPhePheSerThrThrThrLeuThr	100
Db	315 CCTTTGAACCTGGAACATATCAATCTAGTGTATTATTTTCTACGACAACTTGACC	374
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Qy	141 LeuThrAspGlnValValGluGlyGlnTrpGlnTrpValAspAspThrProPheThrGlu	160
Db	495 CTGCACAGACAGGTGGTGGAGGGTCAGTGCNCATGGTGGTGATGATACACCTTTCACAGAG	554
Qy	161 SerLeuSerPheTrpAspAlaGlyGluProAenAenIleValLeuValGluAspCysAla	180
Db	555 TCCCTGAGCTCTCGGATGCTGNNAGACCCCA-CATATAGTTTGGTGGAGGACTGTGCC	613
Qy	181 ThrIleArgAspSerSerAenSerArgLysAenTrpAenAspIlePro	196
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LOCUS	AK036493	
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ACCESSION	AK036493	
VERSION	AK036493.1 GI:26085261	
KEYWORDS	HTC; CAP trapper.	
SOURCE	Mus musculus (house mouse)	
ORGANISM	Mus musculus	
REFERENCE	1. Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.	
AUTHORS	High-efficiency full-length cDNA cloning	
TITLE	Meth. Enzymol. 303, 19-44 (1999)	
JOURNAL	99279253	
MEDLINE	10349636	
PUBMED		
REFERENCE	2. Carninci, P. and Hayashizaki, Y.	
AUTHORS	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes	
TITLE	Genome Res. 10 (10), 1617-1630 (2000)	
JOURNAL		

20499374	MEDLINE
11042159	PUBMED
3	REFERENCE
AUTHORS	
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kiteunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.	
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer	
Genome Res. 10 (11), 1757-1771 (2000)	
20530913	JOURNAL
11076861	MEDLINE
4	PUBMED
REFERENCE	
AUTHORS	
The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.	
Functional annotation of a full-length mouse cDNA collection	
Nature 409, 685-690 (2001)	
5	JOURNAL
REFERENCE	
AUTHORS	
The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.	
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs	
Nature 420, 563-573 (2002)	
6 (bases 1 to 4017)	JOURNAL
REFERENCE	
AUTHORS	
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, I., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.	
Direct Submission	
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)	
CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.	
Please visit our web site for further details.	
URL: http://genome.gsc.riken.jp/	
URL: http://fantom.gsc.riken.jp/.	
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RESULT 7
 BY744630
 LOCUS BY744630 RIKEN full-length enriched, bone marrow macrophage Mus
 DEFINITION BY744630 RIKEN full-length enriched, bone marrow macrophage Mus
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 ACCESSION BY744630
 VERSION BY744630.1 GI:27171386
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 674)
 AUTHORS Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,
 Nikaide, I., Otsu, N., Saito, R., Suzuki, H., Yananaka, I.,
 Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
 Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Buit, C.,
 Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,
 Batalov, S., Beisel, K.W., Blake, J.A., Bradt, V.,

Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A.,
 Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T.,
 Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
 Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A.,
 Kawai, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A.,
 Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,
 Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,
 Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G.,
 Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramchandran, S.,
 Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Shimada, K.,
 Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K.,
 Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M.,
 Varardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,
 Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,
 Wells, C., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,
 Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,
 Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
 Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,
 Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,
 Shingawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,
 Rogers, J., Birney, E. and Hayashizaki, Y.
 Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)

TITLE
 JOURNAL
 MEDLINE
 PUBMED
 COMMENT
 Contact: Yoshihide Hayashizaki
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 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/
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 Genomic Sciences Center and Genome Science Laboratory in Riken.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 tissues were provided by David A. Hume (Depts. of Biochemistry
 and Microbiology/Parasitology Institute for Molecular Bioscience
 University of Queensland Brisbane, Q 4072 Australia) whose
 assistance we gratefully acknowledge.

Please visit our web site (http://genome.gsc.riken.go.jp) for
 further details.

FEATURES
 source
 1. 674
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="1830042L06"
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ORIGIN

Alignment Scores:

Pred. No.: 7,85e-93 Length: 674
Score: 942.00 Matches: 177
Percent Similarity: 98.33% Conservatives: 0
Best Local Similarity: 98.33% Mismatches: 3
Query Match: 79.90% Indels: 1
DB: 6 Gaps: 0

US-10-812-620-2 (1-214) x BY744630 (1-674)

Qy 1 MetAnSerThrIlySerProIaSerHisHieThrGluArgGlyCysPhelyslenSer 20
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Qy 21 GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle 40
|||||
Db 183 CAAGTGCTCTCTGGACGATACCGGGGCTCATCTGTTTCTCAGTGGCTGTTCATC 242
Qy 41 ThrArgCysValValThrTyArgSerSerGlnIleSerGlyGlnAsnLeuGlnProHis 60
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Qy 101 TrpSerSerSerLeuLyAsnCysSerAspMetGlyAlaHisLeuValIleAspThr 120
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Qy 141 LeuThrAspGlnValValGluGlyGlnTrpGlnTrpValAspAspThrProPheThrGlu 160
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Qy 161 SerLeuSerPheTrpAspAlaGlyGluProAsnAsnIleValLeuValGluAspCysAla 180
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Db 603 TCCTTGAGCTTCTGGGATCTGGGAGGCCAACAT-ATAGTTNTGTTGGAGGACTGTGCA 661

RESULT 8

BY749084

LOCUS

BY749084 RIKEN full-length enriched, NOD-derived CD11c +ve dendritic cells Mus musculus cDNA clone F630224E05 5', mRNA

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 655)
Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suihro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
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Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/
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Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

FEATURES

source

1..655
/organism="Mus musculus"
/mol_type="mRNA"
/strain="NOD"
/db_xref="taxon:10090"
/clone="F630224E05"
/cell_type="NOD-derived CD11c +ve dendritic cells"
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ORIGIN

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Score: 936.00 Matches: 175
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Best Local Similarity: 98.87% Mismatches: 2
Query Match: 79.39% Indels: 1
DB: 6 Gaps: 0

US-10-812-620-2 (1-214) x BY749084 (1-655)

Qy 1 MetAenSerThrLysSerProAlaSerHisHthrGluArgGlyCysPheIysAsnSer 20
Db 124 ATGAATTCACCAATCCCTGCATCCACACACAGAGAGAGATGTTCAAAAATCC 183
Qy 21 GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle 40
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Db 304 AGAAATATTAAAGGAGCTTTCTGCTACAGTGGAGCATCAGTTCAGTCAAGAAATGCTGT 363
Qy 81 ProLeuAenTrpLysHisTyGlnSerSerCysTyPhePheSerThrThrLeuThr 100
Db 364 CTTTGGACTGGAACATATCAATAGTTGTTATTTTCTCTACGACAACTTGACC 423
Qy 101 TrpSerSerLeuLysAsnCysSerMetGlyAlaHisLeuValValIleAspThr 120
Db 424 TGGTCATCAAGTTTAAAGAAATGCTCAGACATGGGGCTCACCTGGTGGTTATCGACACA 483
Qy 121 GlnGluGlnGlnPheLeuPheArgThrLysProLysArgLysGluPheTyIleGly 140
Db 484 CAGGAAGAGCAGGAATTCCTTTTTCGCAAAACCTTAAAGGAAGAGTTTATATATGGA 543
Qy 141 LeuThrAspGlnValValGluGlyGlnTrpGlnTrpValAspAspThrProPheThrGlu 160
Db 544 CTGACAGACCAAGTGTGGAGGTCAGTGGCAATGGGTGGATGATACACCTTTACAGAG 603
Qy 161 SerLeuSerPheTrpAspAlaGlyGluProAenAsnIleValLeuValGlu 177
Db 604 TCCCTGAGCTCTGGAGTCTGGGAGGCCCAACAT-ATAGTTTNGTGGAG 653

RESULT 9

BY747821 666 bp mRNA linear EST 17-DEC-2002
LOCUS BY747821.1 GI:27176312
DEFINITION RIKEN full-length enriched, NOD-derived CD11c +ve
dendritic cells Mus musculus cDNA clone F630011J05 5', mRNA
sequence.

ACCESSION

BY747821

VERSION BY747821.1

KEYWORDS GI:27176312

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 666)

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,

Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I.,

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Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,

Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,

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Nature 420, 563-573 (2002)

22354683

12466851

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COMMENT

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RIKEN integrated sequence analysis (RISA) system--384-format

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nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

cDNA library was prepared and sequenced in Mouse Genome

Encyclopedia Project of Genome Exploration Research Group in Riken

Genomic Sciences Center and Genome Science Laboratory in Riken.

Division of Experimental Animal Research in Riken contributed to

prepare mouse tissues.

Tissues were provided by Dr. John Todd (Dept. of Medical Genetics

Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome

Trust/MRC building Addenbrookes Hospital Cambridge) whose

assistance we gratefully acknowledge.

Please visit our web site (http://genome.gsc.riken.go.jp) for

further details.

Location/Qualifiers

1. 666

/organism="Mus musculus"

/mol_type="mRNA"

/strain="NOD"

/db_xref="taxon:10090"

/clones="F630011J05"

/cell_type="NOD-derived CD11c +ve dendritic cells"

/clone_lib="RIKEN full-length enriched, NOD-derived CD11c

+ve dendritic cells"

ORIGIN

Alignment Scores:

Pred. No.: 2.67e-91 Length: 666

Score: 928.00 Matches: 176

Percent Similarity: 97.78% Conservative: 0

Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Akawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																			
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US-10-812-620-2 (1-214) x BY742764 (1-728)

Qy 1 MetaSerThrLysSerProAlaSerHisThrGluArgGlyCysPheLysAsnSer 20
Dd ATGAATTCACAAACAAATCGCTGCATCCACACACAGAGAGAGATGCTTCACAAAACCTCC 183
Qy 21 GluValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle 40
Dd CAAGTGTCTCTCGAGAGATAGCGGGCGCTCCATCTGTTCTTCAGTGGCTGTTTCATC 243
Qy 41 ThrArgCysValValThrTyrArgSerSerGlnIleSerGlyGlnAsnLeuGlnProHis 60
Dd ACCAGATGCTGC----- 255
Qy 61 ArgAsnIleLysGluLeuSerCysTyrSerGluAlaSerGlySerValLysAsnCysCys 80
Dd -----GGTTCAGTCAAGAATTGCTGT 276
Qy 81 ProLeuAsnTrpLysHisTyrGlnSerSerCysTyrPhePheSerThrThrLeuThr 100
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Dd TGGTCATCAAGTTTAAAGAAATGCTCAGCATGGGGCTCACCTGGTGGTTATCGACACA 396
Qy 121 GlnGluGlnGlnGluPheLeuPheArgThrLysProLysArgLysGluPheTyrIleGly 140
Dd CAGGACAGCAGGAGAAATCTCTTTTCGCACAAAACCTAAAGGAAAGAGTTTATATTTGA 456
Qy 141 LeuThrAspGlnValValGluGlyGlnTrpGlnTrpValLeuPheAspThrProPheThrGlu 160
Dd CTGACACAGCAGGTGGTGGAGGGTCAGTGGCAATGGTGGTGGATGATACACCTTTCCACAG 516
Qy 161 SerLeuSerPheTrpAspAlaGlyGluProAsnAsnIleValLeuValGluAspCysAla 180
Dd TCCCTGAGCTCTGGGAGTCTGGGAGCCCAACAT-ATAGTTTNGTGGAGGAGCTGGCC 575
Qy 181 ThrIleArgAspSerSerAsnSerArgLysAsnTrpAsnAspIleProCysPheTyrSer 200
Dd ACCATAGGAGCTCTTC-NACTCCAGGAGAGACTGGATGATATATANCCCTGTTCTACAGT 634
Qy 201 MetProTrpIleCysGluMetProGluIleSerProLeuAsp 214
Dd ATGCTCTGGATTTGTGAGATGCCAGAAATAAGTCTCTCTGGAC 676

RESULT 11

BY743467
LOCUS BY743467 RIKEN full-length enriched, bone marrow EST 17-DEC-2002
DEFINITION musculus cDNA clone I830011F16 5', mRNA sequence.
ACCESSION BY743467
VERSION BY743467.1 GI:27169524
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 645)
Okazaki, Y., Furuno, M., Kasekawa, T., Adachi, J., Bono, H., Kondo, S.,
Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamana, I.,
Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
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PUBMED 12466851
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Email: genome-res@gs.riken.jp, URL: http://genome.gsc.riken.jp/
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10 (11), 1757-1771 (2000)
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cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in Riken.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Tissues were provided by David A. Hume (Depts. of Biochemistry
and Microbiology/Parasitology Institute for Molecular Bioscience
University of Queensland Brisbane, Q 4072 Australia) whose
assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
FEATURES
source 1. 645
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="I830011F16"
/tissue_type="bone marrow"
/cell_type="macrophage"
/clone_lib="RIKEN full-length enriched, bone marrow
macrophage"

ORIGIN

Alignment Scores: 4.13e-90 Length: 645
Pred. No.: 917.00 Matches: 169
Score: 98.83% Conservative: 0
Percent Similarity:

Best Local Similarity:	98.8%	Mismatches:	2
Query Match:	77.78%	Indels:	0
DB:	6	Gaps:	0
US-10-812-620-2 (1-214) x BY743467 (1-645)			
QY	1	MetAenSerThrLysSerProAlaSerHisHisThrGluArgGlyCysPheLysAenSer	20
DB	124	ATGAATTCACCAATTCGGCTCGATCCACACACAGAGAGGATGCTTCAAAAACCTCC	183
QY	21	GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle	40
DB	184	CAAGTGCTCTCTGGACGATAGCCGGGGCTCCATCTGTTCTCAGTGGCTGTTTCATC	243
QY	41	ThrArgCysValValThrTyrArgSerSerGlnIleSerGlyGlnAenLeuGlnProHis	60
DB	244	ACCAGATGTGTGTAACATATCGCAGCTCTCAAAATTCGGGGCAGAACTTACAGCCACAT	303
QY	61	ArgAenIleLysGluLeuSerCysTyrSerGluAlaSerGlySerValLysAenCysCys	80
DB	304	AGAAATATTAAAGAGCTTTCCTGTACGTAGGCGATCAGGTTTCAGTCAAGAAATGCTGT	363
QY	81	ProLeuAenTrpLysHisTyrGlnSerSerCysTyrPhePheSerThrThrThrLeuThr	100
DB	364	CTTTTGAACTCGGAACATTATCAATCTAGTTGTTATTTTCTCTAGGACAACTTGACC	423
QY	101	TrpSerSerSerLeuLysAenCysSerAspMetGlyAlaHisLeuValValIleAspThr	120
DB	424	TGTCATCAAGTTTAAAGAAATTCCTCAGACATCGGGGGCTCACCTGGTGGTTATCGACACA	483
QY	121	GlnGluGluGlnGluPheLeuPheArgThrLysProLysArgLysGluPheTyrIleGly	140
DB	484	CAGGAAGACAGCAAAATTCCTTTTCGCAAAACCTTAAAGAAAGAGTTTATATATGA	543
QY	141	LeuThrAspGlnValValGluGlyGlnTrpGlnTrpValAspAspThrProPheThrGlu	160
DB	544	CTGACAGACAGGTGGTGAGGTCAGTNGCATGGTGGTGATGATACACCTTTCACAGAG	603
QY	161	SerLeuSerPheTrpAspAlaGlyGluProAen	171
DB	604	TCCCTGAGCTTCTGGGATGCTGGGGAGCCCAAC	636
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LOCUS	BY743813		
DEFINITION	BY743813 RIKEN full-length enriched, bone marrow macrophage Mus	643 bp	linear
ACCESSION	BY743813		EST 17-DEC-2002
VERSION	BY743813.1		GI:27170082
KEYWORDS	EST.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
	1 (bases 1 to 643)		
	Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,		
	Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I.,		
	Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,		
	Schyonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C.,		
	Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,		
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Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavoian, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Harai, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yaunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.			
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs			
Nature 420, 563-573 (2002)			
22354683			
12466851			
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Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute			
The Institute of Physical and Chemical Research (RIKEN)			
1-7-22 Suehiro-cho, Teurumi-ku, Yokohama, Kanagawa 230-0045, Japan			
Tel: 81-45-503-9222			
Fax: 81-45-503-9216			
Email: genome-res@gsr.riken.jp, URL: http://genome.gsc.riken.jp/			
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hashizume, W., Hayashida, K., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Saito, R., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Takeda, Y., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y.			
Direct Submission			
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome 12, 673-677 (2001)			
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)			
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)			
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)			
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in RIKEN Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.			
Tissues were provided by David A. Hume (Depts. of Biochemistry and Microbiology/Parasitology Institute for Molecular Bioscience University of Queensland Brisbane, Q 4072 Australia) whose assistance we gratefully acknowledge.			
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.			
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Best Local Similarity:	97.66%	Mismatches:	4
Query Match:	76.76%	Indels:	0
DB:	6	Gaps:	0

US-10-812-620-2 (1-214) x BY743813 (1-643)

Qy 1 MetaSerThrLysSerProAlaSerHisHisThrGluArgGlyCysPheLysAAsnSer 20
 Db 124 ATGAATTCACCAATCGCTGCATCCACCACACAGAGAGAGATGCTTCAAAAACCTCC 183
 Qy 21 GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle 40
 Db 184 CAAATGCTCTCTGGACGATAGCCGGGCGCTCCATCTCTGTTTCTCAGTGGCTGTTCATC 243
 Qy 41 ThrArgCysValValThrTyrArgSerSerGlnIleSerGlyGlnAAsnLeuGlnProHis 60
 Db 244 ACCAGATGTGCTGAACATATCGCAGCTCTCAAAATTCGGGGCAACCTTACAGCCACAT 303
 Qy 61 ArgAsnIleLysGluLeuSerCysTyrSerGluAlaSerGlySerValLysAAsnCysCys 80
 Db 304 AGAAATATTAAAGAGCTTCTCTGCTACAGTGGAGCATCAGGTTCAAGAAATGCTGT 363
 Qy 81 ProLeuSerThrLysHisTyrGlnSerSerCysTyrPhePheSerThrThrThrLeuThr 100
 Db 364 CCTTTGAACCTGGAAACATATCAATCTAGTTGTTATTTTCTCTACGACAACTTGACC 423
 Qy 101 TrpSerSerLeuLeuLysAAsnCysSerAspMetGlyAlaHisLeuValLysAspThr 120
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 Qy 121 GlnGluGlnGlnGluPheLeuPheArgThrLysProLysArgLysGluPheTyrIleGly 140
 Db 484 CAGGAAGAGCAGGAAATCTCTTTTCGCACANAACCTANAGGAAGAGTTTATTTGGA 543
 Qy 141 LeuThrAspGlnValValGluGlyGlnTrpGlnTrpValAspThrProPheThrGlu 160
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 Qy 161 SerLeuSerPheTrpAspAlaGlyGluProAsn 171
 Db 604 TCCCTGAGCTTCTGGGATGCTGGGGGCCCAAC 636

RESULT 13

BY749488
 LOCUS BY749488
 DEFINITION BY749488 RIKEN full-length enriched, B6-derived CD11 +ve dendritic cells Mus musculus cDNA clone F730001C01 5', mRNA sequence.
 ACCESSION BY749488
 VERSION BY749488.1 GI:27178916
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 671)
 AUTHORS Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamana, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K. W., Blake, J. A., Bradt, D., Brusic, V., Clothia, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A., Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A., Kawai, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Konagaya, A., Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W. J., Pertes, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J. C., Reid, J., Ring, B. Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C. A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M., Verardo, R., Wagner, L., Wahlstedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L. G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,

Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S., Rogers, J., Birney, E. and Hayashizaki, Y.
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 Nature 420, 563-573 (2002)
 12466851

TITLE

JOURNAL
 MEDLINE
 PUBMED
 COMMENT

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 The Institute of Physical and Chemical Research (RIKEN)
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 Fax: 81-45-503-9216

Email: genome-res@gscc.riken.jp, URL: http://genome.gsc.riken.jp/
 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hashizume, W., Hayashida, K., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Saito, R., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Takeda, Y., Waki, K., Wataniki, A., Muramatsu, M. and Hayashizaki, Y.
 Direct Submission

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 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
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Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge.
 Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

FEATURES

source

Location/Qualifiers
 1. .671
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 /mol_type="mRNA"
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 /db_xref="taxon:10090"
 /clone="F730001C01"
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ORIGIN

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 Score: 808.00 Matches: 156
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 Best Local Similarity: 85.25% Mismatches: 3
 Query Match: 68.53% Indels: 25
 DB: 6 Gaps: 1

US-10-812-620-2 (1-214) x BY749488 (1-671)

Qy 1 MetaSerThrLysSerProAlaSerHisHisThrGluArgGlyCysPheLysAAsnSer 20
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 Db 124 ATGAATTCACCAATCGCTGCATCCACCACAGAGAGAGATGCTTCAAAAACCTCC 183

QY	21	GinValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle	40
DB	184	CAAGTGTCTCTCTGACGATAGCGGGCCCTCCATCTCTGTCTCAGTGGCTGTTTCATC	243
QY	41	ThrArgCysValValThrTyrArgSerSerGlnIleSerGlyGlnAanLeuGlnProHis	60
DB	244	ACCAGATGTGTCGTAAACATATCGCTGCTCTCAAAATTTCCGGGCAGAACTTTACAGCCACAT	303
QY	61	ArgAanIleLysGluLeuSerCysTyrSerGluAlaSer	73
DB	304	AGAAATATTAGAGACTTTCCTGCTACAGTCAGGCGATCAGGTATAACCATCTGCAGCAC	363
QY	74	-----GlySerVal	76
DB	364	CAGAATCATTAGCAAAAGTTTCGGGCAATGTCTGAAGCCTTTCTCTCTTAGGTTCAGTC	423
QY	77	LysAanCysCysProLeuAanTrpLysHisTyrGlnSerSerCysTyrPhePheSerThr	96
DB	424	AGAATTTGCTGTCCTTTGACATGGGAAACATTATCAATCTAGTGTGTATTTTTTCTCTACG	483
QY	97	ThrThrLeuThrTrpSerSerLeuLysAanCysSerAspMetGlyAlaHisLeuVal	116
DB	484	ACAACCTTGACCTGGTGCATCAAG - TTAAAGAAATTTGCTCAGACATGGGGGCTCACCTGGTG	542
QY	117	ValIleAspThrGlnGluGluGlnGluPheLeuPheArgThrLysProLysArgLysGlu	136
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DB	603	TTTTTATATTGGACTACACACCAGGTGGTGAGGGGTCAATGGGCATGGGATGATACA	662
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LOCUS	BE311916	1032 bp	linear	EST 26-OCT-2000
DEFINITION	601143328f1 NIH_MGC_14	Homo sapiens	CDNA clone IMAGE:3507103 5',	
			mRNA sequence.	

FEATURES

/note="Organ: kidney; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dr priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GCCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using Zap-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Alignment Scores:		
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Best Local Similarity:	65.55%	Mismatches: 42
Query Match:	62.38%	Indels: 7
DB:	2	Gaps: 3
US-10-812-620-2 (1-214)	x BE311916	(1-1032)

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Dd	118	ATGAATTTCATCTAAATCATCTGAAACACAATGCAGACAGAGAGGTGCTTCTTC	174
Qy	21	GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle	40
Dd	175	CAAAATGTTCTTAGACTGTGTCTGGGATCCCATCTATTCTCTCAGTGCGTGTTCATC	234
Qy	41	ThrArgCysValValThrTyrrArgSerSerGlnIleSerGlyGln--AenLeuGlnPro	59
Dd	235	ACCAGATGTGTGTGACATTTCCATCTTCAAACCTCTGATGAGAAAAAGTTTCAGCTA	294
Qy	60	HisArgAsnIleLysGluLeuSerCysTyrrSerGluAlaSerGlySerValLysAenCys	79
Dd	295	CCTGAGAATTTCCACAGAGCTCTCCTGCTCAAAATATGGATCAGGTCAAGTCAAGAA	354
Qy	80	CysProLeuAsnTrpLysHisTyrrGlnSerSerCysTyrrPhePheSerThrThrLeu	99
Dd	355	TGTC CATTTGAACTGGGAATATTTTCAATCCAGCTGCTACTCTCTTTCTACTGACACCAT	414
Qy	100	ThrTrpSerSerSerIleLysAenCysSerAspMetGlyAlaHisLeuValVallIleAsp	119
Dd	415	TCCTGGGCGTGAAGTTTAAGAACTGCTCAGCCATCGGGGCTCACCTGGTGGTTATCAAC	474
Qy	120	ThrGlnGluGlnGlnGluPheLeuPheArgThrLysProLysArgLysGluPheTyrrIle	139
Dd	475	TCACGAGAGAGCAGGAATTCCTTCTCACAGAAACTTAATAATGAGAGAGTTATATT	534
Qy	140	GlyLeuThrAspGlnValValGluGlyGlnTrpGlnTrpValAspAspThrProPheThr	159
Dd	535	GGACTGTGCACACGAGTGTTCGAGGGTCACTGGCAATGGGTGGACGCGACACCTTTGACA	594
Qy	160	GluSerLeuSerPheTrpAspAlaGlyGluProAsnAsnIleValLeuValGluAspCys	179
Dd	595	AAGTCTCTGAGCTTCTGGGATGTAGGGGAGCCCCAACACATAGCATACCTGGGAGGACTGT	654
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RESULT 15
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 IMAGE:3158063, mRNA sequence.
 BX516799 NCI-CGAP_Mam6 Mus musculus cDNA clone IMAGE998G247650 ;
 EXS16799
 ACCESSION
 VERSION
 KEYWORDS
 EST.
 SOURCE
 Mus musculus (house mouse)

RESULT 15
 EXS16799
 LOCUS
 DEFINITION
 486 bp mRNA linear EST 27-JUN-2003
 IMAGE:3158063, mRNA sequence.
 BX516799 NCI-CGAP_Mam6 Mus musculus cDNA clone IMAGE998G247650 ;
 EXS16799
 ACCESSION
 VERSION
 KEYWORDS
 EST.
 SOURCE
 Mus musculus (house mouse)

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 486)
AUTHORS Heil, O., Ebert, L., Neubert, P., Peters, M., Radelof, U., Schneider, D.
and Korn, B.
TITLE Mouse Unigeneset - RZPD2
JOURNAL Unpublished (2003)
COMMENT RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Contact: Ina Rolfs
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD; IMAGp998G247650.
RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
Mouse Unigeneset - RZPD2 (RZPDLIB No.981)
http://www.rzpd.de/CloneCards/cgi-
bin/showLib.pl.cgi?response?libNo=981 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
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Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de

Search completed: June 9, 2005, 16:20:28
Job time : 3183 secs

FEATURES
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/clone_lib="NCI_CGAP Mam6"
/notes="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH"

Alignment Scores:
Pred. No.: 9,92e-70 Length: 486
Score: 730.00 Matches: 135
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Query Match: 61.92% Indels: 0
DB: 5 Gaps: 0

US-10-812-620-2 (1-214) x BX516799 (1-486)

Qy	1	MetAsnSerThrIysSerProAlaSerHisThrGluArgGlyCysPheLysAsnSer	20
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Qy	21	GlnValLeuSerTrpThrIleAlaGlyAlaSerIleLeuPheLeuSerGlyCysPheIle	40
Db	142	CAAGTGTCTCTCGAGAGTAGCCGGGGCTCCATCTCTTCAGTGGCTGTTTCATC	201
Qy	41	ThrArgCysValValThrTyrArgSerSerGlnIleSerGlyGlnAsnLeuGlnProHis	60
Db	202	ACCAGATGTGTGTAACATATCGCAGCTCTCAATTTCCGGCAGAACTTACAGCCACAT	261
Qy	61	ArgAsnIleLysGluLeuSerCysTyrSerGluAlaSerGlySerValLysAsnCysCys	80
Db	262	AGAAATATTAAAGAGCTTCTCTGTACAGTACAGGCATCAGGTTCAAGTCAAGATTGCTGT	321
Qy	81	ProLeuSerTrpLysHisTyrGlnSerSerCysTyrPhePheSerThrThrLeuThr	100
Db	322	CCTTTGAACGTGGAACATTATCAATCTAGTTGTTATTTTCTCTACGAAACCTTGACC	381
Qy	101	TrpSerSerLeuLysAsnCysSerAspMetGlyAlaHisLeuValIleAspThr	120

Db 382 TGTCATCAAGTTTAAAGAAATCTCAGACATGGGGCTCACCTGGTGGTTATCGACACA 441
Qy 121 GlnGluGluGlnGluPheLeuPheArgThrLysProLysArgLys 135
Db 442 CAGGAGAGAGCAGGAGATTCCTTTTTCGCACAAAACCTAAAGAGAAA 486

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